```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

November 8, 2002, 19:24:14 ; Search time 15.0327 Seconds (without alignments) 1470.857 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

NIES .	Description		nypotherical prote	٠.	1 0	A-(a	sase I	e II	endonuclease III (endonuclease III	probable endonucle	probable endonucle	hypothetical prote		O	probable endonucle		ase II	- endonuclease III	ΙΙ	H	probable DNA-(apur	endonuclease-like	endonuclease III (11	Η	endonuclease III		8-oxoquanine-DNA-q	
COLUMNIES	Ü	TABA53	544	D84781	D75275	875373	D84198	G87530	A75109	B69202	F71025	C75459	F72383	T52520	G86758	AF1311	AF1683	B71919	A64593	H70325	B83862	7	32	C69461	in	F71634	B75537	14	9723	
	DB	: `	1 (~	7	7	7	~	~	~	7	~	~	ď	~	~	7	7	7	7	~	~	~	~	~	~	~	~	~	c
	Length	588	917	1207	259	236	265	241	222	233	222	338	232	572	218	219	219	214	218	213	218	264	219	209	219	212	225	297	292	000
æ	Query Match	: ~			ė.	12.9	ä	ď	ς.	'n	11,8	ä	ij.	<u>.</u>	。	ö	10.4	10.1		10.0									8 6.	
	Score	228	201.5	139	112.5	89.5	89.5	٠.	æ	83.5	œ	78.5	7	74.5	74	72	72	20	7	69.5	9	68.5	9	67	9	63.5	ς.	9	61.5	,
	Result Nö.	1	8	m	4	S	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	c

DNA-(apurinic or a	probable endonucle	A/G-specific adeni	adenine glycosylas	adenine glycosylas	DNA-(apurinic or a	cystatin D precurs	endonuclease III X	endonuclease III P	endonuclease III -	endonuclease III -	endonuclease III [endonuclease III P	OGG1 protein - yea	endonuclease III C	A / G specific ade
D98016	6,90,904	B38535	E91108	H85953	A64479	A47142	E82780	н83208	F72387	D70316	AE3104	F98182	S49801	B81407	GB3003
ņ	٧.	N	~	N	~	7	7	~	7	~	7	~	7	~	7
209	117	320	350	350	220	142	218	212	213	220	236	260	376	208	355
		'n	ın	'n	4	e	e	7	ď	~	~	7	7	_	
8.0		00	- :	80	დ	ω ω	ω ω	œ	ω	80	20	80	89	8	œ
61 8.8	00.00	59 8.	59 8.	59 8.	58.5 8.	57.5 8.	57.5 8.	56.5 8.	56.5 8.	56.5 8.3	56.5 8.3	56.5 8.	56.5 8.	56 8.	56 8.

ALIGNMENTS

RESULT 1 1485ULT 1 1490therical protein T32M21.170 - Arabidopsis thaliana Cipocherical protein T32M21.170 - Arabidopsis thaliana Cipocherical Arabidopsis thaliana (mouse-arcfers) Cipocas. 20-Apr 2010 A. Mandris 1. Mardris 2. March 2000 A. Marchelle Collection
--

Dauner D., Herzl A.,

098306; 098306;

RESULT 2 992360

g

```
418 KVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLQGNRK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mewes H.W., Mayer K., Schueller C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021961; CAA17566.1; -.
EMBL; AL161984; CAB80123.1; -.
InterPro; IFR003265; Endo_3c.
InterPro; IFR0035651; Fes_blnd.
                                                            SEQUENCE FECH N.A. Welchard B., Granderath K., Dauner I welchselgarther M. Faxtmann B., Granderath K.Y.; Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       58.9%; Score 162; DB 10; 343.9%; Pred. No. 1.3e-19; tive 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                     Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  onservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 43; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 091269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             091260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  datches
                                                                                                                                                                                                                                                                                                                                                  SMART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09LZ69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
      සි
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA,

MEDLINE-20083487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Fujii C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umman M. K., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Sequence and analysis of chromosome 2 of the plant Arabidopsis

thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Moyse-ear cress).

Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosida II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXERXXFXXXXXXTXRWXXXQGXR 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 59.5%; Score 163.5; DB 10; Length 1207; Local Similarity 43.4%; Pred. No. 9.7e-20; les 43; Conservative 0; Mismatches 47; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006919; AAD24633.1; -
InterPro; IPR003651; Fes_bind.
SMART; SM00555; FES; 1.
SEQUENCE 1207 AA; 135916 WW; ADDB6C9EE94DDF67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 106.3 kps protein.
F28A23.180 OR AT4G34060.
                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               560 RFTPWKGSVVDSVVGVFLTQNVSDHLSSSAFMSLASQFP 598
          53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      917 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                 At2936490 protein.
```

Query Match

Matches

5

Gaps

., 8

Indels

Length 917;

```
Arabidopsis thaliana (Mouse-ear Cress).

Bukaryota, Whitdiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KVXXDXXTAXXXXXXXXXXXXXXXXXXX-----XXERXXFXXXXXXXFIXRMXXXQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             931 KVDIDDETT¶IWNLLMGKGDEKEGDEEKDKKKEKWWEEERRVFRGRADSFIARMHLVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 33; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h | 18.0%; Score 49.5; DB 10; Length 1017; Simifarity 28.8%; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     017 AA; 112139 MW; 4F7C313A891EC83F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL162875; CAB85562.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                          01-0CT-2006 (TrEMBLrel. 15, Created)
01-0CT-2006 (TrEMBLrel. 15, Last sequence update)
01-0CT-2006 (TrEMBLrel. 15, Last annotation update)
01-0CT-1006 (TremBLrel. 15, Last annotation update)
132M21_160.
                                                                 478 FKQWKGSVVDSVVGVFLTQNTTDYLSSNAFMSVAAKFP 515
54 FXXWKGBVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                    PRT; 1017 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
```

Ĥ

RESULT 5

Dauner D.,

I.M., Weichselgartnef M., Fartmann B., Granderath K., Dauner

SEQUENCE FROM N.A.

NCBI_TaxID=3702;

049498

RESULT 3 049498

g

셤 à

ò

```
controlled asse III - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
C;Accession: B69202
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oliu, D.S.; Schurch, G.M.; Daniels, C.J.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; S.; Church, G.M.; Daniels, C.J.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; S.; Church, G.M.; Daniels, C.J.; Mathanobacterium thermoautotrophicum Delta H.; A.; Accession: B69202
A;Accession: B69202
A;Accession: B69202
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-233 <MTH>A;Residues: 1-244 MTH
A;Residues: 1-244 MTH
A;Residues: 1-245 MTH
A;Residues: 1-245 MTH
A;Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable endonuclease III - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Dacces: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Daccession: F71025
R;Rawarabayaai, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
R;Rawarabayaai, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-222 <KAW>
                                      A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49586.1; PID:g545
A;Experimental source: strain Orsay
C;Genetics:
A;Genetics:
C;Genetics:
C;Superfamily: apurinic/apyrimidinic endonuclease III
C;Keywords: 4Fe-45; metalloprotein
F;195,202,205,211/Binding site: 4Fe-45 cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 12.4%; Score 86; DB 2; Ler
Best Local Similarity 26.9%; Pred. No. 1.2e-05;
Matches 29; Conservative 11; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.0%; Score 83.5; DB 2;
Best Local Similarity 26.9%; Pred. No. 3.1e-05;
Matches 29; Conservative 10; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: MTH764
A;Start codon: TTG
C;Superfamily: apurinic/apyrimidinic endonuclease III
    A; Residues: 1-222 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endonuclease III family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: G87530
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D.J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Froc. Nati. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Accession: G87530
A;Status: preliminary
A;Accession: DNA
A; DNA
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: A75109
R;Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: A75109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 <STO>
A;Cross-references: GB:AE004437; NID:g10580010; PIDN:AAG18952.1; GSPDB:GN00138
C;Genetics:
A;Gene: nthAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-241 csro>
A; Residues: 1-241 csro>
A; Cross-references: GB:AE005673; NID:913423785; PIDN:AAK24243.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KXXLLXXXGXGLKSXECVRLLXLXX-XAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLX 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 GXIDLEWLRXXXXXXXXXXXLLXXXGXGLKSXECV-RLLXLXXXXAFPVDTNVGRIXVRXGX 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 VPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXX 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V-----GSGDTTNTYHTLMAMAPASW-----TADDLFELHWLMKRGLGQMLCGAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 AVPDAA------CGFG------HTAMIQFGR-EYCTARDPACLDDPAACPL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 XYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNC----NACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endonuclease III (nth) PAB0459 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73; Indels
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: D84198
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.9%; Score 89.5; DB 2;
Best Local Similarity 27.6%; Pred. No. 3.9e-06;
Matches 32; Conservative 8; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 12.5%; Score 86.5; DB 2; 1 Similarity 24.2%; Pred. No. 1.1e-05; 31; Conservative 9; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 PNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CC2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

÷

Gaps

```
Cipecies: Neurospora crassa
Cipacies: Oct-2000 #sequence_revision 20-Oct-2000
Rischulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, September 2000
A: Reference number: 226053
A: Reference number: 226053
A: Recession: T52520
A: Seculation preliminary
A: Molecule type: DNA
A: Residues: 1-572 <SCH>
         A;Accession: F72383
A;Status: preliminary
A;Molecule type: DnA
A;Rosidues: 1-232 <ARN>
A;Esidues: 1-232 <ARN>
A;Esidues: 1-232 <ARN>
A;Esperimental source: SE:AE001718; GB:AE000512; NID:g4980881; PIDN:AAD35467.1; PID:g498
C;Genetics: A;Genetics: Strain MSB8
C;Genetics: A;Genetics: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
G86758
NNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) [imported] - Lactococcus li
NNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) [imported] - Lactococcus li
N.Alternate names: endonuclease III
C;Species: Lactococcus lactis subsp. lactis
C;Accession: G86758
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, R.; Weissenbach, J.; l
Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 NLSRLRDLPTHILRERLLKIKGIGKETADAILLYALEKPVFVVDSYTRRLLKRIFNIELN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 XGXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLC--KLXQXTLYELHYXXITFGKXXF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---CDVKVPDHLKYGLHQLFIRHGQQCF 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 DLEWLRXXXXXXXXXXLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLX 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 PLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EDVRLYQEFHGLIVEHAKKFCSK-TPKCG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 VXXXGXIDLEWLRXXXXXXXXXXLXXXGLKSXECVRLLXLXXXAFPVDTNVGRIXVR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL442164; GSPDB:GN00116; NCSP:B2J23.160
A;Experimental source: BAC clone B2J23; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68; Indels

    Neurospora crassa

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%; Score 74.5; DB 2; 24.1%; Pred. No. 0.0018; ive 10; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 76; DB 2;
Pred. No. 0.00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein B2J23.160 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 -C-----TKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537 KCRKATRPGTKEWREAPECPL 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.0%;
ilarity 22.5%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 DY-DEVOKLFMTHYP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496 LGWVPEKANAEDCFRH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 ACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 VCPLKKECC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: NCSP: B2J23.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable endonuclease III - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Oilore 1999 #sequence_revision 03-Dec-1999 #text_change 31-mar-2000
C;Aucession: C75459
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Recession: C75459
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: Draiminary
A;Draiminary
A;Drai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F72383
hypothetical protein TM0382 - Thermotoga maritima (strain MSB8)
Species: Thermotoga maritima
C;Species: Thun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72383
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
    A;Cross-references: GB:AP000006; NID:gaisaiss, Figuressian.
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Gene: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PH1498
C;Superfamily: apurinic/apyrimidinic endonuclease III
C;Superfamily: apurinic/apyrimidinic endonuclease III
C;Keywords: 4Fe-45; iron-sulfur protein; metalloprotein
F;195,202,205,211/Binding site: 4Fe-45 cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec
A;Keference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
Cross-references: GB:AP000006; NID:93236133; PIDN:BAA30606.1; PID:93257923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 GXIDLEWLRX----XXXXXXXKXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 RXGXVPLXPLPXXXQXHXLXXYPXXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGLSLRFLREFPHTPEGHEQARQALAALPGVGHKTVALVLLFDLRRPAMPVDGNMERAAK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%; Score 78.5; DB 2; 22.7%; Pred. No. 0.00026; iive 14; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                 11.8%; Score 82; DB 2; 26.9%; Pred. No. 5.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 TKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 RSKHPLCPQCPL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
C75459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

딥

- Lactococcus lac

٠.

Gaps

```
C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #text_change 14-Dec-2001
C; Accession: AF1311
C; Daninguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
C; Acuthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G; Maddeno, E.; Maitournam, A.; May Actubras: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Tille: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AF1311
A; Status: prediminary
A; Molecule type: DNA
A; Residues: 1-219 cGLA
A; Rosicules: Strain EGD-e
C; Genetics:
A; Experimental source: strain EGD-e
C; Genetics:
A; Superfamily: apurinic/apyrimidinic endonuclease III
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable endonuclease III (DNA repair) [imported] - Listeria monocytogenes (strain EGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                       A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-218 <270>
A:Cross-references: GB:AE005176; PID:912724026; PIDN:AAK05169.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: nth
C:Superfamily: apurinic/apyrimidinic endonuclease III
C:Keywords: carbon-oxygen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 KKVLOTLPGVGRKTANVVLAEAYGIPGIAVDTHVERVSKRLDIVP------- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 GVGRKTANVVLSVGFGVPAIAVDTHVERISKRLGICRWKDSVVEVEETLKRKLP----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 KXXLLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXX 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 GXGLKSXECVRLLXLXXXAFPVDTNVGRLXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 YPXXXXXQKX----LWPRLCKLX-QXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74; DB 2; Length 218;
Pred. No. 0.00092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72; DB 2; Length 219;
Pred, No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 KXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 KELWS------DAHHYMIFFGR-YHCKARNPECPTCPL 201
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.7%; Score 74; DB 3
Best Local Similarity 25.9%; Pred. No. 0.000
Matches 30; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
10.4%; Score 72; DB 3
Best Local Similarity 25.2%; Pred, No. 0.003
Matches 26; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: November 8, 2002, 19:26:43 Job time : 17.0327 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

.. ش

Gaps

45;

Indels

Length 259;

```
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Cispecies: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Cispecies: 03-Feb-2001 #sequence_revision 02-Feb-2001
Cispecies: 03-Feb-2001 #sequence_revision 02-Feb-2001
Cispecies: 03-Feb-2001 #sequence_revision 03-Feb-2001
Cispecies: 03-Feb-2001 #text_change 02-Feb-2001
Cispecies: 03-Feb-2001 #text_change 03-Feb-2001
Cispecies: 03-Feb-2001 #text_change 03-Feb-2001
Cispecies: 03-Feb-2001 #text_change 03-Feb-2001
Cispecies: 03-Feb-2001
Cis
A; Accession: D75275
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-259 <WHI>
A; Residues: 1-259 <WHI>
A; Cross references: GB: AE002073; GB: AE000513; NID: 96460244; PIDN: AAF11977.1; PID: 9646
C; Genetics: A; Gene: DR2438
A; Gene: DR2438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 112.5; DB 2;
; Pred. No. 8.7e-10;
10; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 PRMGEQAAHRALLALLPPDPPY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 ITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: |: | | | | | | 210 LSHGR-OVCTWTRPKCGKC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 25.2%;
Matches 35, Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
D84198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
S75373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ρp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. Accession: D84781
R.Lin, X.: Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Mcffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Merman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A.71tle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUD:20083487; PMID:10617197
A.Accession: D84781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.J.;
C.; Ma
                                                                                                                                                           695
                                                                                                            A;Map position: 4
A;Introns: 41/3; 70/3; 88/1; 118/1; 321/1; 367/1; 474/1; 504/2; 624/3; 655/2; 667/3; A;Introns: 41/3: 180
C;Superfamily: Arabidopsis thaliana hypothetical protein F28A23.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gispecies: Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Objective: Ob
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein At2936490 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 VDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYX 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----YELHYQ 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKTRSTMDTVDWKAIRAADVKEVAETIKSRGMNHKLAERIOYLTLNMKIMOGFLDRLVND 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 XGXIDLEWLRXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGX 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 VPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXIIFGKXXFCTKXX 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PDKAK-----YELHYQMITFGK-VFCTKSK 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                      Length 917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.1%; Score 139; DB 2; Length 1207; 25.1%; Pred. No. 2.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                           Query Match 29.1%; Score 201.5; DB 2; Best Local Similarity 49.5%; Pred. No. 2.2e-23; Matches 46; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 XITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 25.1 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             906 HGSIDLEWLR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        917 VP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
Matches 5
                                                                        C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
probable DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - Sulfolobus solfat N:Alternate names: endonuclease III; protein c04006 (Species: Sulfolobus solfataricus C:Species: Sulfolobus solfataricus C:Species: Sulfolobus solfataricus C:Date: 09-oct-1997 #sequence_revision 24-oct-1997 #text_change 20-Jun-2000 (SAccession: S75373 R:Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, Mol. Microbiol. 22, 175-191, 1996 A:Title: Organizational characteristics and information content of an archaeal genome A:Reference number: S73076; MUID:97055432; PMID:8899719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: 1-236 <SEN>
A.Status: 1-236 <SEN=
A.Status: 1-236 <ASTATUS A.Status: 1-236 <ASTATUS A.Status predicted
C.Superfamily: apurint-Zapyrimidinic endonuclease III
C.Staywords: 4Fe-4S; carbon-oxygen lyase: metalloprotein
F;204,211,214,219/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                    91 LLXXXGXGLKSXECVRLL---XLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXX 147
GXIDLEWLRXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXV 131
                                                                                                                                                                                    P------LXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXX 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 YPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 YSLISSTLKELF----SAYDLLHLHHMLIAHGRQT-CKARKPLCNSC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 12.9%; Score 89.5; DB 2; Best Local Similarity 27.5%; Pred. No. 3.5e-06; Matches 30; Conservative 9; Mismatches 49;
```

Herzl A.,

098JQ6 098JQ6;

RESULT 2

쇰

```
418 KVNLDPETIKEWDVLMVNDBPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLQGNRK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                   --XXXXDXXXXXXXXXERXXEXXXXXXXXIXRMXXXQGXRX 53
                                                                     Fartmann B., Granderath K., Dauner D., H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021961; CAA17566.1; --
EMBL; AL161584; CAB8(4123.1; --
                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                          106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Score 162; DB 10;
Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 FKQWKGSVVDSVVGVFLTQNTTDYLSSNAFMSVAAKFP 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
   Mewes H.W., Mayer K., Schueller C.;
Submitted (FEB-1998≯ to the EMBL/Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/G.
EMBL; ALI62875; CAB85562.1;
Hypothetical protein.
SEQUENCE 1017 AA; 112139 WW; 4:
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                  Endo_3c.
Fes_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.0%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                            58.98;
43.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KVXXDXXTXXXWXXL---
                                                                                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                  InterPro; IPR003265;
InterPro; IPR003651;
Pfam; PF00730; HhH-GP
                                                                                                                                                                                                                                                                                    SMART; SM00478; ENDO3
SMART; SM00525; FES;
                                                                                       Neumann S., Mewes H.
Submitted (MAR-2000)
                                                      SEQUENCE FROM N.A. Weichselgartner M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        Hypothetical
SEQUENCE 91
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09LZ69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09LZ69
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
Q9LZ69
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20083487; PubMed=10617199; Lin X. Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Eujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Niermen W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; Salzberg S.L., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-eat cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eldicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacea; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 KVDLDDETDRVWKLLLENINSEGVDGSDEQKAKWWEEERNVFRGRADSFIARMHLVQGDR 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 163.5; DB 10; Length 1207;
Pred. No. 9.7e-20;
0; Mismatches 47; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDB C9EE94DDF67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/Genhank/DDBJ databases
                                                                                                                                          Créated)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     date)
560 RFTPWKGSVVDSVVGVFLTQNVSDHLSSSAFMSJASOFP 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXRAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          049498;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
Hypothetical 106.3 kDa protein.
F28A23.180 OR AT4G34060.
                                                                                                          PRT; 1207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC006919; AAD24633.1; -.
InterPro; IPRO03651; FeS_bind.
SMART; SM00525; FES; 1
SEQUENCE 1207 AA; 135916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.5%;
                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                At2g36490 protein.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
```

thaliana

ä

Gaps

8

Indels

Length 917;

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702; 931 KVDIDDETTRIWNLLMGKGDENGEGDEEKDKKKEKWWEEERRVFRGRADSFIARMHLVQG 989 Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Vah Montagu M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. Length 1017; Indels NW; 4F7C313A891EC83F CRC64; KMBL/GenBank/DDBJ databases 01-077-2000 (TrEMBLrel. 1b, Created) 01-077-2000 (TrEMBLrel. 1b, Last sequence update) 01-077-2000 (TrEMBLrel. 1b, Last annotation update) Hypothetical 112.1 KDa prptein. DB 10; 33; Score 49.5; Di Pred. No. 9.4; g δ

RESULT

Dauner D.,

DUBNCE FROM N.A. San, M., Welchselgartner M., Fartmann B., Granderath K., Nooll N., Neumann S., Hoheisel J., Jesse T., Helinga-b, V

F

049498

RESULT 3

q

දු ŏ

ó

049498

Matches

```
November 8, 2002, 19:24:15; Search time 11.1765 Seconds (without alignments) 1659.222 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-840-743-71
275
1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671580
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_21:*
1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fung1:*
4: Sp_human:*
5: Sp_huwan:*
6: Sp_nammal:*
7: Sp_nammal:*
7: Sp_phage:*
7: Sp_phage:*
7: Sp_phage:*
7: Sp_vorganelle:*
7: Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0.
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                      Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		Qysrob arabidopsis	09s1q6 arabidopsis	049498 arabidopsis	091z69 arabidopsis	009617 caenorhabdi	09d223 mus musculu	09v4c2 homo sapien	Opppt3 ureaplasma	Opfng3 arabidopsis	Ogp3u0 schizosacch	Q9sz60 arabidopsis	09c9v5 arabidopsis	093yu0 arabidopsis	O8zw64 pyrobaculum	Q8rwm5 arabidopsis	Q9c9e0 arabidopsis
ID		CASKOO	09SJQ6	049498	09LZ69	009617	090223	Q9Y4C2			_		Q9C9V5	093YU0	Q8ZW64	O8RWM5	036360
DB	!	2	10	10	10	'n	11	4	16	10	m	10	10	10	17	10	10
% Duery Match Length DB		1203	1207	917	1017	541	207	921	1131	373	1141	327	738	765	120	128	217
% Query Match		2.00	59.5	58.9	18.0	17.1	16.7	16.7	16.4	16.2	16.0	15.8	15.8	15.8	15.6	15.6	15.6
Score	3 331	7.00	163.5	162	49.5	47	46	46	45	44.5	44	43.5	43.5	43.5	43	43	43
Result No.	-	4	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16

Q9k9zl bacillus ha Q9bkl3 paramecium Q91948 arablidopsis Q929e3 listeria in Q8y544 listeria mo Q98y64 septembla Q9x0v8 thermotoga P87638 deague viru Q8q160 olive leaf Q9bpz homo sapien Q9nuzl homo sapien Q9nuzl homo sapien Q9nuzl homo sapien Q9tv2 homo sapien Q9tv2 homo sapien Q9tv2 homo sapien Q9tv3 klebsiella Q9tv3 corva sativ Q9tv3 corva sativ Q9tv3 corva sativ Q9tv3 corva sativ Q9tv3 arabidopsis Q9c833 arabidopsis Q9c833 arabidopsis Q9c833 arabidopsis melseejemyce	026841 methanobact 090wg2 gallus gall 09p9b4 uncultured
09K9Z1 09BK13 092LV81 092LV81 092E3 08Y544 0029BD6 0029BD6 003PBD6 009KD0 09BPZ2 09BPZ2 09BPZ2 09BPZ2 09BPZ2 09BPZ2 09BPZ3 09BPZ	O26841 O90WG2 D9P9B4
	200 000
	~~~
23 30 40 40 40 40 40 40 40 40 40 4	255 265 31
n n n n n n n n n n n n n n n n n n n	4.4.4 o.o.o.
	177
44444444444444444444444444444444444444	4 4 4 1 1 1 1
1111 0222222222222222222222222222222222	4 4 4 5 4 4

## ALIGNMENTS

5;

53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90

δ

a

Ĥ

Gaps

PRELIMINARY;

**091268** 

RESULT 2 Q9LZ68 ID Q9LZ0

931

셤

ò 셤

```
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                 37 IXXRGXÄXXLXXRIXXXXXXXXXXXFLXXXVXXXGXIDLEWLRXXXXXXXXXXLLXXXG 96
                                                                                                                                                                                                                                                                                        31 IKERGMNNYLAKRI-----KDFLNRLVREHGNIDLEWLRDVPPDKAKEYLLSIRG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 VDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQRXLWPRLCKLXQXTLYELHYX 1.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dauner D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---YELHYQ 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herzl A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.\
Bevan M., Weichselgartner M., Fartmann B., Granderath K., Dauner
Bevan M., Neumann S., Hoheisel J., Jesse T., Heijnen L., Vos P.,
Mewes H.W., Mayer Kl., Schueller C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                          Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A. Weichselgartner M., Fartmann B., Granderath K., Dauner D., Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                   Asada T., Fukusaki E., Kobayashi A., Sando T., "Prenyltransferase of Euphorbia tirucalli."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AB051105; BAB47587.1; InterPro; IPR003265; Endo_3c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021961; CAA17546.1;
EMBL; AL161584; CAB80129.1;
InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; Fed_bind.
                                                                                                                                                                  FBDBCE4CD0CC5B81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                               Score 202; DB 10;
Pred. No. 8.1e-26;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                  97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXP 135
                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 201.5; DB 1
Pred. No. 7.8e-25;
                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 XITFGKXXFCTKXXPNCNACPMXXXEÒXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             625 VDTNVGRIAVRLGLVPLEPLPNGVQNHQLFE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Cree 01-JUN-1998 (TrEMBLrel. 06, Last 01-JUN-2001 (TrEMBLrel. 17, Last Hypothetical 106 3 kDa protein. F28A23.180 OR AT4G34060.
                                                                                                                                             119 119
119 AA; 13771 MW;
                                                                                                                                                                                                   29.1%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.18;
                                                                                                          Pfam; PF00730; HhH-GPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 917 AA, 106310
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELJIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 49.5
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00478; ENDO3c;
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00730; HhH-GPD;
                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                  50;
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           049498
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                         049498
                         RA
RI
DR
DR
DR
FT
                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                  930
                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplandae; Streptophyta; Embryophyta; Tracheophyta; Sperimtophyta; Magnolipphyta; eudicotyledons; core eudicots; Rosidae; NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVRI------KDFLERIVKDHGGIDLE 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 WLRXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Rosidae; mossidae; Malpighiales; Euphorbiaceae; Euphorbia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
SEQUENCE FROM N.A.

Bevan M., Terryn N., Ardales W., Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
Villaroel R., Glelen J., Van Montagu M., Bancroft I., Mewes H.W.,
Sudmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                  157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA
                                                                      61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVARDIdopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL162875; CAB85563.1;
InterPro; IPR003265; Endo_3c,
Ffam; PF00730; HhH-GFD, 1
SMART; SM00478; ENDO3c, 1.
Hypothetical protein.
SEQUENCE 555 AA; 62088 MW; AIB44BDDE17FDCIE CRC64;
                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 62.1 kPp protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 228; DB 10;
Pred. No. 1.6e-29;
0; Mismatches 61;
                                                                                                                                                                                   555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119, AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up-
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Putative FPPsynthasel (Fragment).
                                                                                                                                                                                 PRT;
```

3;

Gaps

PRT;

PRELIMINARY;

094LX6; Q94LX6

RESULT 3 Q94LX6

Euphorbia tirucalli.

ETFPPS1

ROM N.A.

436 DSIDYEAIRRASISEISEAIKERGMNNM

g ð g à

138 XXXQXHXL 145

546 ESLQLHLL 553

0;

57; Conservative

Similarity

Query Match Best Local Matches 5

32.9%;

SEQUENCE! FROM N.A.

7

# GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

using sw model protein search, OM protein 8, 2002, 19:24:15; Search time 28.5621 Seconds November Run on:

(without alignments) 1659.222 Million cell updates/sec

US-09-840-743-72

score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 , Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_vertebrate:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_archea:*
sp_bacteria:*
sp_fung1:* sp_organelle:* sp_phage:* sp_rodent:* sp_virus:* sp_plant:* SPTREMBL_21:* sb_mhc:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Ogsr66 arabidopsis					Ogrra0 deinococcus				09a623 caulobacter			026858 methanobact		059167 pyrococcus	
	De							, Di	0	<i>)</i>			0		0	,,	0
	OI .	09SR66	Q9LZ68	094LX6	049498	902860	O9RRO0	P95945	Q9HS56	Q9P9L7	09A623	9M0V6Q	0801н8	026858	<b>0971F2</b>	059167	Q9RVU4
	,	10	10	10	10	10	16	17	17	17	16	17	17	17	17	17	16
	Match Length DB	1309	555	119	917	1207	259	236	265	223	241	222	225	233	224	222	338
* Ouerv	Match	48.4	32.9	29.1	29.1	20.1	16.2	12.9	12.9	12.6	12.5	12.4	12.1	12.0	12.0	11.8	11.3
	Score	335,5	228	202	201.5	139	112.5	89.5	89.5	87.5	86.5	86	84	83.5	83	83	78.5
Result	No.	1	7	m	4	S	9	7	8	6	10	11	12	13	14	15	16

Q9wyl3 thermotoga Q8r957 thermoanaer Q9hfi6 neurÖspora Q9cgms lactococcus Q8tha8 methanosarc	Q92ab4 listeria in Q8y608 listeria mo Q8ty08 methanopyru Q8ty408 methanopyru Q92+20	2921p6 helicobacte Q921p6 helicobacte Q25307 helicobacte O66636 aquifex aeo O9kc76 bacillus ha		Q81vm6 methanopyru Q97aj2 thermoplasm Q91cri paenibacill Q9vih0 drosophila Q9vih1 deinococus	09cbj0 mycobacteri 097fm4 clostridium 097qe0 streptococc 09w592 drosophila 097173 clostridium 098gul rhizobium l
5 Q9WYL3 Q8R957 Q9HFI6 5 Q9CGM5			a	0.0	097EM4 097EM4 0970E0 0970E0 097L73 097L73
		214 16 218 16 213 16 218 16	264 17 219 16 220 2 282 17		297 16 292 16 209 16 1072 5 211 16 238 16
11.0 10.8 10.8 10.7	10.4	100.1	999999		8888888 998877
76 74.5 74.5 72.5	72 72 70.5	70 70 69.5	68.5 68 68 67.5	66.5 64.5 64 63 63	62 61.5 61 60.5 60.5
17 18 19 20 21	22 23 24 25	28 28 29 29	30 33 33 44	38 3 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	44440 012845

### ALIGNMENTS

CSTRAIN-CV. CCLUMBIA;

CA STRAIN-CV. CCLUMBIA;

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,

Rabidopsis thaliana chromosome III BAC T22X18 genomic sequence.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; AC010927; AAF04422.1; -.

RICHEPTO; IPR003265; Eas.bind.

RICHEPTO; IPR003365; Ees.bind.

REAMST; SM00478; ENDO35; I.

RAMART; SM00478; ENDO35; I.

SWART; SM00478; ENDO35; I.

SWART; SM00478; ENDO35; I.

SWART; SM00425; FES; I. Length 1309; 56; Indels DB 10; ch 48.4%; Score 335.5; DB 1 1. Similarity 47.4%; Pred. No. 3.1e-47; 82; Conservative 0; Mismatches 56 PRT; 1309 AA PRELIMINARY; Query Match Best Local Similarity **09SR66** RESULT 1 Q9SR66 ò a

4

97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXXPXXXXXQK 156

ò

Search completed: November 8, 2002, 19:28:34 Job time : 14.1765 secs

oy Dp

```
SEQUENCE FROM N.A.

Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
Yamada K., Banh J., Banno F., Chang C., Toriumi M., Wu H.C.,
Yamamura Y., Yu G., Wu S., Bowser L., Carninci P., Chen H., Cheuk R.,
Hayashizaki Y., Ishida J., Jones T., Ramiya A., Karlin-Neumann G.,
Rawai J., Kim C., Koesema E., Lam B., Lin J., Mayers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
Ecker J.R., Theologis A.;
"Full Length conno of gene At1967890 (GI:15220577).";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.6%; Score 43; DB 17; Length 120; 38.9%; Pred. No. 12;
Live 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00086; PAC; 1.
TIGREAMS; TIGR00229; sensory_box; 1.
PROSITE; PS50011; PROTEIN_KINASE_bom; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
ATP-binding; Hypothetical protein; Transferase.
SEQUENCE 765 AA; 85149 MW; 6651738FB4E347D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL. AE009849; AAL63838.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 120 AA; 13398 MW; 34DP06D06226AD5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAE1954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 78;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43.5;
                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR001610; PAC.
InterPro; IPR001014; PAS domain.
InterPro; IPR002090; Ser_thr_pkinase.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed-11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 RGNLIQSPFGVFLC-NDDKSSSKA 355
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 KGSVVDSVXGVFLTQNXDXXSSXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoproteaceae; Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 FXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.8°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 38.5.
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=13773;
                                                                   NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aerophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAE1954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8ZW64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     082W64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    082W64
    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                        Theologis A., Ecker J.R., Palma C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
A Chung M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., Dewar K.,
A Chung M.K., Conn L., Conway A.B., Choway A.B., Fujii C.Y.,
A Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
A Lin S.X., Liu S.X., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A Hiltscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I.,
A Rakano H., Salzerg S.L., Schwartz J.R., Shinn P., Town C.D.,
Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Town C.D.,
A Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
W "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surenatophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR00229; sensory_box; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 408:816-820(2000).

-- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; AC012563; AAG52018.1; --

HSSP; P12931: IFMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     738 AA; 82220 MW; B2B65569A52D6145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 85.1 kDa protein.
ATIG67890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   765 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.8%; Score 43.5; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000014; PAS domain.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MEDLINE-21016719; Pubmed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 RGNLIQSPFGVFLC-NDDKSSSKA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001610; PAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 KGSVVDSVXGVFLTQNXDXXSSXA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAC.
PAS_domain.
Hypothetical 82.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00086; PAC; I.
SMART; SM00091; PAS; I.
SMART; SM00220; S_TKC; I.
SMART; SM00219; TYFKC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00785; PAC; 1
Pfam; PF00989; PAS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
```

Query Match

Matches

qq δλ

Q93YU0; Q93YU0

RESULT 13
093YU0
1D 093YU
AC 093YU
DT 01-DE
DT 01-DE
DF HYPOT
GN AT1GG
OS Arabi

ij

Gaps

1;

Indels

8;

ö

Gaps

; 0

ö

```
SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mowes H.W., Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         э;
Э
                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     Score 44; DB 3; Length 1141;
Pred. No. 99;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL360054; CAB96001.1; -.
InterPror; IPR001394; UCH-2.
Pfam; PF00443; UCH-1; 1.
PROSITE; PS00972; UCH-2; 1.
PROSITE; PS00973; UCH-2.1; 1.
PROSITE; PS00973; UCH-2.2; 1.
                                                                                                                                                                    1499E32DB6CB26CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO49538; CAB40936.1; -.
EMBL; ALO45533; CAB78238.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ll protein.
327 AA; 35845 MW; B2BB47DF4A83E635 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypotheitcal 35.8 kDa protein.
F16013.20 OR AT4G11950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                   327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               738 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.8%; Score 43.5; 41.7%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 GGGKLSRWKVAVGSVIGSIIGAFL 267
                                                                                                                                                                                                                                                                                                                       882 KQTLYDALDGVFETVNIDMGSETA 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 GXRXFXXWK---GSVVDSVXGVFL 70
                                                                                                                                                                    1141 AA; 130296 MW;
                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                  58 KGSVVDSVXGVFLTQNXDXXSSXA
                                                                                                                                                                                                           16.0%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 17, TrEMBLrel. 17, TrEMBLrel. 21,
                                                                                                                                                                                                           Ouery Match 16.0
Best Local Similarity 41.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (
01-JUN-2001 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
SEQUENCE 32
                                                                                                                                                    Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9C9V5
Q9C9V5;
                                                                                                                                                                                                                                                                                                                                                                                                                   092560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
Q9C9V5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                   092560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H H H H H
       οy
                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II. Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned P1 clones.";
DNA Res. 4:291-300(1997).
BMBL; AB006696; BAB103741. -.
SEQUENCE 373 AA; 41666 MW; 48B8C3396A9832D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=COLUMBIA;
MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=972H-;
Saunders D., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
.,
                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 373;
                                                                                                                                                                                                           DB 16; Length 1131;
     "The complete sequence of the mucosal pathogen Ureaplasma
                                 Mature 407:757-762(2000).

BMBL; AE002154; AAF30970.1; -.

EMBL; AE0021547; GLS.

InterPro; IPR001547; GLS.

Pfam; PF00496; SBP_bac_5.

PROSITE; PS00659; GLYCOSYL HYDROL_F5; UNKNOWN_1.

Hypothetical protein; Complete protecome.

SEQUENCE 1131 Aa; 130078 WW; C45DBBF61E18690B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPAC128.06.
Schlzosaccharomyces pombe (Fission yeast).
Bukaryota; Fungl; Ascomycota; Schlzosaccharomycetes; Schlzosaccharomycetales; Schlzosaccharomycetales; Schlzosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase.
                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44.5; DE
Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                         Score 45; DB 1
Pred. No. 66;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 WKGRIVDSATPSEFNGEFLAQ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 WKGSVVDSVX----GVFLTQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.2%;
47.6%;
                                                                                                                                                                                                           16.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                     744 FDKYAGSTYDSALGLFLT 761
                                                                                                                                                                                                                                                                                    54 FXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                           Local Similarity 50.0
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tabata S.;
                                                                                                                                                                                                         Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9P3U0
Q9P3U0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        09FNQ3;
                                                                                                                                                                                                                                                                                                                                                                                                               COSFNQ3
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
```

RESULT 9

õ qq **09FNQ3** 

Π

÷

09P3U0

٥y g

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIAA0738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Y4C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PPT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
            DR
DR
SQ
                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alaxawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsud H.A., Ashburner M., Batalov S., Casavant T., Sakai K., Okido T., Fassi C., King B., Kochiwa H., Sakai K., Okido T., Furuni L.M., Raduli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Rownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wilttaker C., Wilming L., Mashima Y., Kawaji H., Kohtsuki S., Hasseyawa Y., Kawaji H., Kohtsuki S., Hasseyawa Y., Kawaji H., Kohtsuki S., Haspashizan P., Marshiona J., Kawaji H., Kohtsuki S., Haspashizan P., Marshiona J., Kawaji H., Kohtsuki S., Haspashizan J., Marshiona J., Kawaji H., Kohtsuki S., Haspashizan J., Marshiona J., Kawaji H., Kohtsuki S., Haspania J., Marshiona J., Kawaji H., Kohtsuki S., Haspashizan J., Marshing L., Kawaji H., Kawashi J., Marshing L., Kawaji W., Kawaji H., Kahtaki K., Kawai M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.1%; Score 47; DB 5; Length 541; 28.2%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z48638; CAA88567.1; -.
WormPep; ZK892.3; CE01726.
                                                                      01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 61.0 kDa protein ZK892.3 in chromosome II.
ZK892.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 AA; 61045 MW; A7A1D7EDB140AC6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 RIFSNWANARILVVEVAFITRRWDTASYVCAAISALIFP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001589; Actbind_actnin.
InterPro; IPR003662; sub_transporter.
Pfam; PF000083; sugar_tr; 1.
PR05TTE; PS00019; ACTININ_1; UNKNOWN_1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 RXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                         541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 13;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=HYPOTHALAMUS; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, A230020K05Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 28.2 les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                       Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 541 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A230020K05RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lloyd C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                      009617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    090223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q09617

LD Q00

DT Q00

DT Q01

DT Q01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large protelins in vitro.";
DNA Res. 5:277-286(1998).
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SEROVAR 3;
MEDLINE=20500219; Pubmed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                      DB 11; Length 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 921;
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO182B1; BAA34458.1; -.
EMBL; BC000609; AAH00609.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03D39FDF90561F74 CRC64;
EMBL; AK020704; BAB32184.1; -.
MGD; MGI:1924824; A230020K05Rik.
SEQUENCE 207 AA; 22411 MW; 558A70EC798BB4C9 CRC64;
                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical membrane lipoprotein.
                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                     6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1131 AA.
                                                                                                                                                                                                                                                                 921 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                         Mismatches
                                                                      Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 RXFXXWKGSVVDSVXGVFLTQNXDXXS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99087487; PubMed=9872452;
                                                                                                                                                               921 AA; 102139 MW;
                                                                                                                                      52 RXFXXWKGSVVDSVXGVFLTQN 73
                                                                    16.7%;
40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.7%;
                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2002 (TrEMBLrel. 21,
                                                 Query Match
Best Local Similarity 40.30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE OF 1-919 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     KIAA0738 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                              09Y4C2; 09BW63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-SKIN;
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9L269;
Q9L269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09LZ69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRARRER RAP REPRIED BRANKER RAPARA REPRIED BRANKER REPRIED BRANKER REPRIED BRANKER REPRIED BRANKER REPRIED BRANKER BRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CY. COLUMBIA;
MEDLINE-20083487; Pubbed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo, H., Moffat K.S.,
Cronin L.A., Shen M., VanAens S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXERXXFXXXXXXXXXIXRMXXXQGXR 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dauner D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-2001 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 106.3 kba protein.
F28A23.180 OR AT4G34060.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Wagnollophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bevan M., Weichselgartner M., Fartmann B., Granderath K., Dauner
Herzl A., Neumann S., Hoheisel J., Jesse T., Heijnen L., Vos P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 1207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135916 MW; ADDB6C9EE94DDF67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 163.5; DB 1
Pred. No. 9.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          917 AA
                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                   PRT; 1207
                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AC006919; AAD24633.1; -. InterPro; IPR003651; Fes_bind. SMART; SM00525; FES; 1. SEQUENCE 1207 AA; 135916 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%;
                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin X.;
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                        At2g36490 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   049498
                                                                                                                                                                                      901860
                                                                                                                        RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
049498
                                                                                                                                                                                         IDD BREEF READ BREEF R
                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     පු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
```

```
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 KVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLQGNRK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVDIDDETTRIWNLLMGKGDEKEGDEEKDKKKEKWWEEERRVFRGRADSFIARMHLVQG 989
                                                                                                              Herzl A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXXERXXFXXXXXXXIXXXXQXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,

Bec Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,

Villaroel R., Gielen J., Wondagu M., Bancroft I., Mewes H.W.

Rudd S., Lemcke K., Mayer K.F.X.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KVXXDXXTXXXWXXLXXXXDXXXXXXXX-----XXERXXFXXRXXXXFIXRMXXXQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  917;
                                                                                                              Dauner D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL162875; CABB5562.1; -.
Hypothetical protein.
SEQUENCE 1017 AA; 112139 WW; 4F7C313A891EC83F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;

EU Arabidopsis sequencing project;

EMBL, AL021961; CAA17566.1;

EMBL, AL021964; CAA17566.1;

InterPro; IPR003265; Endo_3c.

InterPro; IPR003265; Endo_3c.

InterPro; IPR003651; FeS_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
Mewes H.W., Mayer K., Schueller C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                     Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l protein.
917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 112.1 kba protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.0%; Score 49.5; DB 10;
11arity 28.8%; Pred. No. 9.4;
Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                 SEQUENCE FROM N.A.
Weichselgartner M., Fartmann B., Granderath K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.9%; Score 162; DB 10; 43.9%; Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 43.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
```

1;

5

Q9k9z1 bacillus ha

09bk13 paramecium

Q929e3 listeria in Q8y544 listeria mo

Q9p8d6 aspergillus Q23010 caenorhabdi

0933KB Klebsiella 08uee5 agrobacteri 09fvn0 lycopersico 09kry9 vibrio chol 09zta4 arabidopsis 09rc22 becillus sp

Q9x0v8 thermotoga P87638 dengue viru Q8q160 olive leaf

homo sapien homo sapien

09bpz2 Q9nuz1 Q9jy82 neisseria m O26841 methanobact Q90wg2 gallus gall Q9p9b4 uncultured

5

> g δ

δλ

arabidopsis 09c9v5 arabidopsis 093yu0 arabidopsis OBzw64 pyrobaculum OBrwm5 arabidopsis O9c9e0 arabidopsis

09zs60

QBRWM5 Q9C9E0

093YU0 Q8ZW64

100

43.5 43.5 43.5 43 43

44.5 44

53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90

Q9c903 arabidopsis Q9c833 arabidopsis Q91kp0 dengue viru Q9xce9 streptomyce

O9hhx9 halobacteri O94dv2 oryza sativ Q17748 caenorhabdi

```
STRAIN-CV. COLUMBIA;

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,

Bowman C.L., White O. Nierman W.C., Fraser C.M.;

"Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence.";

I. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC010927; AAF04422.1;

R. InterPro: IPR003265; Endo.3c.

InterPro: IPR003651; FeS_bind.

R. Pfan: PF00730; HH-GPD; 1.

R. SMART; SM00478; ENDO37; 1.

R. SMART; SM00525; FES; 1.

O SEQUENCE 1309 AA; 148451 MW; 3B21E4439BA4A673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids II; Brassicales: Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.5%; Score 166.5; DB 10;
43.4%; Pred. No. 3.2e-20;
ive 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                            Q9X0V8
P87638
Q8QL60
Q9BPZ2
Q9NUZ1
Q93GK8
              Q9BK13
Q9LV81
Q929E3
Q8Y544
                                                                                                                                                                                                                          Q9FVN0
Q9KRY9
Q9ZTA4
Q9KC22
Q9HX9
Q94DV2
Q17748
                                                                                                                                                                                                                                                                                                                                                     Q9C833
Q91KP0
Q9XCE9
                                                                                                                                                                                                                                                                                                                                                                                                     Q9JY82
O26841
Q90WG2
Q9P9B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                               Q9P8D6
Q23010
                                                                                                                                                                                             10
10
10
10
                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
291
723
777
777
777
777
780
281
282
311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     t Local Similarity
ches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T22K18.18 proteiņ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
1155.6
1155.6
1155.6
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
1155.3
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
 T22K18.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9SR66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
 09SR66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9sr66 arabidopsis O9sig6 arabidopsis O49498 arabidopsis O91269 arabidopsis O91617 caenorhabdi O96223 mus musculu O994c2 homo sapien O9ppt3 ureaplasma O9fnq3 arabidopsis O9p3u0 schizosacch
                                                                                                        2002, 19:24:15; Search time 11.1765 Seconds (without alignments) 1659.222 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number of results predicted by chance to have a an or equal to the score of the result being printed, y analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                       275
1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP
                                                                                                                                                                                                                                                                                                                       671580
             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SR66
Q9SJQ6
Q49498
Q9LZ69
Q005617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PPT3
Q9FNQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               092260
090000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      090223
                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9P3U0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
                                                                                                                                                                                                                                                                                                                                                   length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
16
3
                                                                                                                                                                        US-09-840-743-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_archeap:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL 21:*
                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1309
1207
917
1017
541
1131
1131
132
738
765
120
120
                                                                                                            November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       %
Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.5
59.5
58.9
18.0
17.1
16.7
```

Post-processing:

Database

sed

Minimum DB Maximum DB

Perfect score:

Run on:

Sequence:

Scoring table:

Pred. No.

166.5 163.5 162 49.5

Score

Result ٠ 9

ΟŊ

Search completed: November 8, 2002, 19:28:38 Job time : 32.5621 secs

9

```
STRAIN=OT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus,
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                059167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                      STRAIND-ELTA H. S. SMITCAGE T. DECUGHERY C., Lee H.-M., Dubois J., A. Aldredge T., Bashirzadeh R., Dalakely D., Cook R., Gilbert K. A. Aldredge T., Bashirzadeh R., Wierzbowski J., Gibson R., A. Jiwan I., Keagle P., Lumm W., Pothier B., Qiu D., Radafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwan I., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G. Goyal A., Pietrovski S., Church G.M., A. Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; T. Complete genome sequence of Methanobacterium thermoautotrophicum and ysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).

S. Balt. AED008855, AABBS SG7.1; J. S. SHIMEL, AED008855, AABBS SG7.1; J. S. SHIMER ST. SHOO356; Endo.3c. InterPro; IPR003565; Endo.3c. InterPro; IPR003565; Endo.3c. InterPro; IPR003569; HHH.1. SRWART; SM00578; HHH.1. SWART; SM00578; HHH.1. I. SWART; SM00578; HHH.1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.; "Complete genome sequence of an aerobic thermoacidophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 LLXXXGXGLKSXECVRLLXLXXXAFPUDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 LLKLPGVGRKTANCVLVYAFGRPAIPVDTHVHRISNRIGLVD-TRTPEETERALMKVIP- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 83.5; DB 17; Length 233; Pred. No. 1.4e-05;
                                                                                                Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----REYW-----IELNDLMVQFGQ-DICRPLGPRHEECPI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endonuclease; Complete proteome.
SEQUENCE 233 AA; 27012 MW; 10F6163AAE98395B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative endonuclease III.
01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                Methanobacteriaceae; Methanothermobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.0%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-JCM 10545 / 7;
PubMed-11572479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ST1401.
Sulfolobus tokodaii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus.
NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=187420;
                                                  Endonuclease III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0971F2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q971F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
Q971F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
DPT COCCOS ON THE COCCOS ON TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98344137; Pubbmed=9679194;

Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Sakai M., Ogura K., Otsuka B., Nakazawa H., Takamiya M., Ohiuku Y.,

Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Aoki K. -I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

Masuchi Y., Shizuya H., Kikuchi H.,

"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";

DNA Res. 5.55-76[1998].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 LLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 LXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXX 151
                                                                                                                                                                                                                                                                                                                                                                                                             18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                         Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 222;
Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL; AP000986; BAB66468.1; -
InterPro; IPR003265; EndoIII_FCL.
InterPro; IPR003265; EndoIII_FCL.
InterPro; IPR003285; HH4.1.
Ffam; PF00730; HH4.63p; 1.
Ffam; PF00730; HH41; 1.
FROSITE; PS00764; ENDONUCLEASE_III_1; UNKNOWN_1.
Findonuclease; Hypothetical protein; Complete proteome.
SEQUENCE 224 AA; 25629 MW; E2BE3A0762135550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
11.8%; SCULE 02, 2. Best Local Similarity 26.9%; Pred. No. 2.4e-05;
Matches 29; Conservative 10; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 XXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD096F91C969DF0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ol-Aug-1998 (TrEMBLrel. 07, Created) 01-Aug-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 222AA long hypothetical endonuclease III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; UNKNOWN_1.
Endonuclease; Complete protections Complete protection 222 As, 25553 MM; DD096F91C969DF0C (
                                                                                                                                                                                                                                                                                                                                                            12.0%; Score 83; DB 17; 25.7%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004035; EndoIII_HhH.
InterPro; IPR00356; Endo_3c.
InterPro; IPR003551; FeS_bind.
InterPro; IPR003583; HHH_1.
Ffam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00278; HES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P20625; 2ABK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=53953;
```

4;

_ _ _ _ _ _ _

S

```
*Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                               InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004036; EndoIII_HhH.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003561; HHH_I.
Pfam; PF00730; HHH-GPD; I.
SMART; SM00478; ENDO3c; I.
SMART; SM00278; HHHI; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 25.9%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            026858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8U1H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   026858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
026858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEATAIN-ATCC 19989 / CEB15;

MEDLINE-21173698; PubMed-11259647;

MISTRAIN-ATCC 19989 / CEB165;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

R. Sien J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

POLOCKA I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

POLOCKA I., Nelson W.J., Durkin A.S., Gwinn M.L., Haft D.H.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Ralzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

IL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 GXIDLEWLRXXXXXXXXXXXLLXXXGXGLKSXECV-RLLXLXXXAFPVDTNVGRIXVRXGX 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 VPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXX 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 GWLSLSHLKTLEVDQARWELQALPGVGVKVAACVLNFSDLAMRALVVDTHVDRVARRIGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 V-----GSGDTTNTYHTLMAMAPASW-----TADDLFELHWLMKRGLGQMLCGAEA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
162 EKYDEISRW-FMERLPRDKYLDFHLKLIQFGR-DVCRARNPKCGQCPI-GAKCPSFKSA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.5%; Score 86.5; DB 16; Length 241; 24.2%; Pred. No. 4.5e-06; ive 9; Mismatches 73; Indels 15;
                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AA; 26421 MW; EB43FBA976736F1C CRC64;
                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Endonuclease III family protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 AA
                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; CC2272; -.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; Fes_bind.
Pfam; PF00730; HhH-GPD; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Endonuclease III (NTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.55
Best Local Similarity 24.23
Matches 31; Conservative
                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                          Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 PNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 PKCGACPV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus.
NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTH OR PAB0459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ORSAY;
Heilig R.;
                                                                                                                                                                                                                                                                                                                                         Caulobacter.
                                                                                                                                             Q9A623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9W0V60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
09900W
AC 0900W
AC 0900W
DT 01-MA
DT 0
                                                                       RESULT 10
                                                                                              Dp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 LIKLPGIGRKCANIVLAYGFGIPAIPVDTHVYRISRRLGLAPWDASPEEVEERL----- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus furiosus.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus genome."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB010230; AAL81353.1; -. Complete proteome. SEQUENCE 225 AA; 26157 MW; DA48762AC33EE4AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --EILKTLIP-----VEEWIY-VNHAMYDHGK-SICRPIKPKCELCPL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 -----KELIPR-----EEWIY-VNHAMVDHGK-SVCRPIKPRCDECPL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
Structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ7482B5; CAB49586.1; --
HSSP; P20625; 2ABK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25541 MW; 27F0B5FC838C0DC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycosylase putative, mutY-nth family.
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; UNKNOWN_1.
Endonuclease; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17;
5.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.1%; Score 84; DB 17; 25.9%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 12.4%; Score 86; DB Local Similarity 26.9%; Pred. No. 5.1e les 29; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches
```

```
--
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                  265 AA;
                                                                             Query Match
Best Local Similarity
            Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAE0880
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9P9L7
                                                                                                                                                                                                                        145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                              Q9P9L7
         SO
                                                                                                                                                                           ŏ
                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                            HDD COCCOOR SERVING TO DESCRIPTION OF SERVING THE SERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,
"The complete genome of the crenarcheon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
EMBL: AR06650; AAK40470.1; --
HSSP: P20625; ZABK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20504483: PubMed=11016950;
MEDLINE-20504483: PubMed=11016950;
MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithuser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennits P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 LLXXXGXGLKSXECVRLL---XLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXX 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.9%; Score 89.5; DB 17; Length 236; Best Local Similarity 27.5%; Pred. No. 1.4e-06; Matches 30; Conservative 9; Mismatches 49; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 YPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 YSLISSTLKELF-----SAYDLLHHHMLIAHGRQT-CKARKPLCNSC 214
                                                                                                                                                                                                                                                        InterPro; IPR003565; EndoIII_FCL.
InterPro; IPR003565; Endo_3c_
InterPro; IPR003565; Endo_3c_
InterPro; IPR003565; Endo_3c_
InterPro; IPR003565; Endo_3c_
InterPro; IPR003583; HHH.1.
R Pfam; PF00730; HhH-GPD; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00278; HhH1; 1.
R PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
R PROSITE; Lyase; Complete protecome.
SEQUENCE 236 AA; 26843 MM; 6FF5CADB280ECCD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
EMBL; AE004996; AAG18952.1; -.
HSSP; P20625; ZABK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro: IPR003265; Endo_3c.
Interpro: IPR003651; FeS_bind.
Interpro: IPR003693; HHL_1.
Interpro: IPR000408; Reg_chr_condens.
Pfam; PF00730; HH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
SMART; SM00278; HHH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTHAL OR VNG0398G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endonuclease III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HS56
Q9HS56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95SH60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٥y ،
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
```

```
2:
                                                                                               5,
                                                                                                                                             88 KXXLLXXXGXGLKSXECVRLLXLXX-XAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLX 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of a thermostable DNA glycosylase specific for U/G and T/G mismatches from the hyperthermophilic archaeon Pyrobaculum aerophilum.";
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative DNA glycosylase (DNA-(apurinic or apyrimidinic site) lyase)
(endonuclease III, PaNKh)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AF222334; AAF37269.1; -.
EMBL; AE009791; AAL63095.1; -.
                                                                                                                                                                         147 XYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNC----NACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fitz-Glbbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-20138151; Pubmed=10671447;
Yang H., Fitz-Gibbon S., Marcotte E.M., Tai J.H., Hyman E.C.,
Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.6%; Score 87.5; DB 17; Length 223; 26.9%; Pred. No. 2.8e-06;
                                              Length 265;
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
CEFB1A2A1DB9735E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyase, Endonuclease, Complete proteome.
SEOUENCE 223 AA; 25323 MW; 8A8445E9462167E3 CRC64;
                                                                                            53;
                                           Score 89.5; DB 17;
Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00764; ENDONUCLEASE_III_1; UNKNOWN_1.
                            12.9%; Sco...
27.6%; Pred. No. 1...
... 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed-11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 182:1272-1279(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P20625; 2ABK.
InterPro; IPR004035; EndoIII_FCL.
InterPro; IRR003265; Endo_3c.
InterPro; IPR003561; FeS_bind.
InterPro; IPR003581; HHH_1.
Pfam; PF00730; HHH_2CPD; I
27481 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoproteaceae; Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
SMART; SM00278; HhH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                            Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
```

m

```
SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA;

MEDLINE=20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L.J., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Salzberg S.L., Fraser C.M., Venter J.C.;

Salzberg S.L., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    917 VP----YDRAK------PDKAK-----YELHYQMITFGK-VFCTKSK 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 XGXIDLEWLRXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGX 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 VPLXPLPXXXQXHXLXXXPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXX 190
                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         846 EKTRSTMDTVDWKAIRAADVKEVAETIKSRGMNHKLAERIQYLTLNMKIMOGFLDRLVND 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.1%; Score 139; DB 10; Length 1207; 25.1%; Pred. No. 3.4e-14; ive 0; Mismatches 65; Indels 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDB6C9EE94DDF67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AA
                                 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC006919; AAD24633.1; -. InterPro; IPR003651; Fes_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 PNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                943 PNCNACPM-KGECRHFASA 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

Best Local Similarity 25.14
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402:761-768(1999).
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0525; FES;
1207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             906 HGSIDLEWLR----
                                                                                                                   At2g36490 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endonuclease III.
DR2438.
                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM(
SEQUENCE
                                 90rs60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9RROO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
Q9RRQ0
RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OC OS DIT
                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
```

.,

```
Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,
Doolittle W.F., Ragan M.A., Charlebois R.L.,
"Organizational characteristics and information content of an archaeal
genome: 156 kb of sequence from Sulfolobus solfataricus P2.";
Mol. Microbiol. 22:175-191(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 GXIDLEWLRXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-----LXPLPXXXQXHXLXXYPXXXXQKXLWPRLCKLXQXTLYELHYXX 177
                                                              MEDLINE=20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.2%; Score 112.5; DB 16; Length 259; 25.2%; Pred. No. 2.1e-10; Live 10; Mismatches 49; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
                                                                                                                                                                                                    "Genome sequence of the radioresistant bacterium Deinococcus radiodurans \mathrm{R1."}\,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Endonuclease III (DNA endonuclease III, probable) (NTH-1)
                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00764; ENDONUCLEASE_III_1; 1.
Endonuclease; Complete proteome.
SEQUENCE 259 AA; 28946 MW; AA07354719093547 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-97055432; Pubmed-8899719;
                                                                                                                                                                                                                                                                                        InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR003565; Endo_3c.
InterPro; IPR003651; Fes_bind.
PFM PF00730; HHH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
                                                                                                                                                                                                                               Science 286.1571-1577(1999).
EMBL; AE002073; AFF11977.1; -.
TIGR; DR2438; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 ITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 LSHGR-QVCTWTRPKCGKC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 25.2%;
Watches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTH-1 OR SSO0116 OR C04006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2287;
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EC 4.2.99.18)
                                                                                                                                                                                           Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P95945
P95945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
P95945
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
```

٠. ش a

```
eurosids II; Bra
NCBI_TaxID=3702;
                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          049498
049498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     049498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
  RA BRE BRE DR DR DR DR ETT SO
                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                  930
                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 WLRXXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euphorbia tirucalli.
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 DSIDYEAIRRASISEISEAIKERGMNNMLAVRI------KDFLERIVKDHGGIDLE 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarcol R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.9%; Score 228; DB 10; Length 555; 44.5%; Pred. No. 1.6e-29;
                                                              157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA
                                                                                        ------ELYELHYHMITFGK-VFCTKVKPNCNACPM-KAECRHYSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL162875; CAB85563.1;
Interpro; IRR003265; Endo_3c.
Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
Hypothetical protein.
SEQUENCE 555 AA; 62088 MW; AlB44BDDE17FDC1E CRC64;
                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 62.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative FPPsynthasel (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 XXXQXHXL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 ESLOLHLL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                            eurosids II; Bra
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  094LX6;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                      09LZ68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q94LX6
                                                                                                        931
                                                                                                                                                                       RESULT 2
091268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
Q94LX6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDT AND DDT AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                  g
                                                              ò
                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
```

```
3;
                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 VDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYX 1.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Varidiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YELHYQ 661
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dauner D., Herzl A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                            37 IXXRGXXXXLXXXXXXXXXXXXXXXXVXXXGXIDLEWLRXXXXXXXXXLLXXXG
                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Bevan M., Weichselgartner M., Fartmann B., Granderath K., Dau
Herzl A., Weuchon S., Hoheisel J., Jesse T., Heljnen L., Vos
Mewes H.W., Mayer K., Schueller C.;
                                                                                                                                                                                                                                                                   Length 119;
Asada T., Fukusaki E., Kobayashi A., Sando T.;
"Prenyltransferase of Euphorbia tirucalli.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO51105; BAB47587.1;
InterPro; IRR003265; Endo_3c.
Pfam; PF00730; HHH-GPD; 1.
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL021961; CAA17566.1; -.
EMBL; AL05184; CAB0123.1; -.
InterPro; IPR002565; Endo_3c.
InterPro; IPR003651; PeS_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weichselgartner M., Fartmann B., Granderath K., Dauner Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                               FBDBCE4CD0CC5B81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 106.3 kDa protein.
F28A23.180 OR AT4G34060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 8.1e-26;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXP 135
                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.1%; Score 201.5; DB 1
49.5%; Pred. No. 7.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   662 MITFGK-VFCTKTIPNCNACPM-KSECKYFASA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 XITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                 Score 202;
                                                                                                                                                                                                                  119 AA; 13771 MW;
                                                                                                                                                                                                                                                                   29.1%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00478; ENDO3c; 1. SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                               Best Local Similarity 50.5
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00730; HhH-GPD;
                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
```

Q9wyl3 thermotoga Q8r957 thermoanaer

Q9hfi6 neurospora

O9cgm5 lactococcus O8tha8 methanosarc

Q92ab4 listeria in Q89ab4 listeria in Q8408 listeria mo Q84yu8 methanopyru Q92t20 rhizobium m Q92lp6 helicobacte C05307 helicobacte C05636 aquifex aeo Q9kc76 bacillus ha Q9yfvO aeropyrum p Q99u37 staphylococ Q8tk57 methanopyru Q8181 archanosarc C28581 archanopyru Q97aj2 thermoplasm

097qe0 streptococc 09w592 drosophila 097173 clostridium 098qu1 rhizobium 1

Q9rxml deinococcus Q9cbj0 mycobacteri Q97fm4 clostridium

091cri paenibacill 09vih0 drosophila

4

832 IIKRGMNNMLAERI-----KAFLNRLVKKHGSIDLEWLRDVPPDKAKEYLLSING 881 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXXQXHXLXXYPXXXXXQK 156

97

37

ŏ

methanobact

Score

Result Ño. 026858 0971f2 059167 09rvu4

deinococcus sulfolobus pyrococcus

g οý

IXXRGXXXXLXXRIXXXXXXXXXXXXXFLXXXXXXXXGXIDLEWLRXXXXXXXXXXXXC 96

7

Perfect score:

Sequence:

,

OM protein

ou :

Run

Scoring table:

Searched:

Minimum DB Maximum DB

Database

```
PEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA,
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Lin X., Kaul S., Town C.D., Benito M.C., Fresheck T.R., Barnstead M.E.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraz Kill genomic sequence.";
T. Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence.";
L. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC010927; AAF04422.1;
R. InterPro; IPR003265; Ens. Jind.
R. InterPro; IPR003365; Ens. Jind.
R. SMART; SM00478; ENDO3c; I.
R. SMART; SM00478; ENDO3c; I.
R. SMART; SM00525; FES; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1309 AA; 148451 MW; 3B21E4439BA4A673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 335.5; DB 1 Pred. No. 3.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                    Q9LCR1
Q9VIH0
Q9RXM1
Q9CBJ0
Q97FM4
Q97CE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                          Q8TYU8
Q92T20
Q92LP6
O25307
O66636
                                                                                                                                                                                                        Q9YEV0
Q99U37
Q9EUT1
                                                                                                                                                                                                                                                       Q8TK57
O28581
Q8TVM6
Q97AJ2
                                              Q9CGM5
Q8THA8
                                                                               Q92AB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                               16
16
16
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T22K18.18 protein.
T22K18.18.
                                                                                                                                           1100.1
1100.1
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.
                                                                                                                                                                                                                                                                                      27880000H2
                                                                                                          70.5
                                                                                                                                                                          69.5
69
                                                                                                                                                                                                                                                       67.5
67
                                                                                                                                                                                                                                                                                   66.5
64.5
64
                                                                                                                                                                                                                                                                                                                                                  62.5
                                                                                                                                                                                                                                                                                                                                                                                                                                60.5
                                                           72.5
                                                                                                                                                                                                                                                                                                                                                                                   61.5
                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                       68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9SR66
Q9SR66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
098R66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9sr66 arabidopsis
Q91z68 arabidopsis
Q941x6 euphorbia t
Q9498 arabidopsis
Q9rrg deinococcus
P95945 sulfolobus
Q9hs56 halobacteri
Q9p917 pyrobaculum
Q9a623 aculobacteri
Q9V0W6 pyrococcus
Q8v1h8 pyrococcus
                                                                                                          2002, 19:24:15; Search time 28.5621 Seconds (without alignments) 1659.222 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                    671580
              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                   671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                091268
0941x6
049498
095306
098R00
P95945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09P9L7
09A623
09V0W6
08U1H8
026858
0971F2
059167
                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mhc:*
sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_archeap: *
                                                                                                                                                                US-09-840-743-72
693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
110
110
110
110
110
110
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_fungi:*
sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sb_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
                                                                                                             November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448
332
3333
3333
3333
1122
1122
1122
1123
1133
1133
1133
1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
```

```
Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: H72278

A;Accession: Preliminary

A;Molecule type: DNA

A;Residues: 1-832 <ARN>
A;Cessorseferences: GB:AE001779; GB:AE000512; NID:94981777; PIDN:AAD36306.1; PID:9498

C;Genetics:
                                                                                                                      Tipha mannosidase-related protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72278
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicgartett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.
Ayîtle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; PMID:11743193
A;Accession: AE2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE008688; PIDN:AAL42811.1; PID:g17740257; GSPDB:GN00186 A;Experimental source: strain C58 (Dupont) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.3%; Score 42; DB 2; Length 432;
.larity 31.0%; Pred. No. 38;
Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ed. No. 52;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8, 2002, 19:26:41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 KAKIVSPIDGVILTRSVDPGATVASSLNA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 KGSVVDSVXGVFLTQNXDXXSSXAXMXXA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: Atul815
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||| :| ||||
160 WKGSDGTAVQGVFL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 WKGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: November
Job time: 8.88235 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Status: preliminary
A Molecule type: DNA
A: Residues: 1-432 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: TM1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Д
                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Listeria innocus control in the control 
                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein homolog lin2334 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL592022; PIDN:CAC97561.1; PID:g16414857; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-565 <GRE>
A;Residues: 1-565 <GRE>
A;Cross-references: EMBL:U64853; PIDN:AAB04976.1; GSPDB:GN00023; CESP:K11G9.1
A;Experimental source: strain Bristol N2; clone K11G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein K11G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T29718
R;Greco, T.; Bradshaw, H.
Submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid K11G9.
A;Reference number: 220672
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
9
                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 434;
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 5
A;Introns: 31/3; 114/3; 144/2; 282/1; 352/1; 460/1
C;Superfamily: cholinesterase; cholinesterase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 WKGSVVDSVXGV-----FLTQNXDXXSSXAXMXXAXXF 89
                                                                   5;
                                                             Score 43; DB 2
Pred. No. 26;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 43; DB
ilarity 57.1%; Pred. No. 26;
Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43;
Pred. No.
C; Superfamily: hypothetical protein HI0107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: lin2334
C;Superfamily: hypothetical protein HI0107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.6%;
30.8%;
                                                             15.6%;
ilarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||::|||||||:
386 VDTIGGWFLTQNYE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11:: | ||||| :
386 VDTIGGWFLTQNYE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 VDSVXGVFLTQNXD 75
                                                                                                                                                                                       62 VDSVXGVFLTQNXD 75
                                Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: K11G9.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

ö

Gaps

ö

Length 832; 4; Indels

5; DB ö

Gaps ; 0

```
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: C96748
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-294 <STO>
A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06222.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ridlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jonnes, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Tiele: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-434 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00310.1; PID:916411702; GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein lmo2232 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE005173; NID: 96730759; PIDN: AAF27148.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BH2503 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 RYLPTWKGNVIDAEMEMNPGHVVGMSLSVNAQGGGFIGAKSGAGDF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 RXFXXWKGSVVDS-----VXGVFLTQNXDXXSSXAXMXXAXXF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: BH2503
C;Superfamily: conserved hypothetical protein HI1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 2;
Pred. No. 17;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.6%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGSVVDSVXGVFLTQNXD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                                                         A; Residues: 1-217 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: G83962
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: AH1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: G83962
                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: T10D10.11
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: 1mo2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
hypothetical protein F16J13.20 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 23.4pr-1999 #sequence_revision 23-4pr-1999 #text_change 22-Oct-1999
C; Accession: T06602
R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 1999
A; Accession: T06602
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-327 < AEEv>
A; Residues: 1-327 < AEEv>
A; Cross-references: EMBE:AL049638; GSPDB:GN00062; ATSP:F16J13.20
A; Experimental source: cultivar Columbia; BAC clone F16J13
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pypothetical protein T23K23.26 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: D2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F96701
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Anaute 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, A;Authors: Salzaberg, S.L.; Schwartz, J.B.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: F96701
A;Astatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown protein T10D10.11 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96748
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ransen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 916-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE005173; NID:g6553906; PIDN:AAF16572.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.8%; Score 43.5; DB 2; Best Local Similarity 41.7%; Pred. No. 16; Matches 10; Conservative 2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.8%; Score 43.5; 45.8%; Pred. No. 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 GGGKLSRWKVAVGSVIGSIIGAFL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGNLIQSPFGVFLC-NDDKSSSKA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 GXRXFXXWK---GSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 KGSVVDSVXGVFLTQNXDXXSSXA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-738 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Gene: T23K23.26
A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
F96701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
```

I Ø

ö

Gaps

ö

Indels

ij

Gaps

8;

ö

Gaps

ö

g οy q

ð

```
hypothetical protein UU557 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: F92875 F;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein ZK892.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28069
R;Lloyd, C.
R;Lloyd, C.
A;Reference number: 220465
A;Reference number: 220465
A;Reference number: Library, March 1995
A;Reference number: 220465
A;Reference number: 220463
A;Referen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.1%; Score 47; DB 2; Length 541; 28.2%; Pred. No. 6.8; ive 4; Mismatches 24; Indels
                                                                                                                                                                                      Length 442;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 RXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 2
A;Introns: 45/1; 105/2; 199/3; 303/2; 382/3; 503/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 RTFSNWANARILVVFVAFITRRWDTASYVCAAISALIFP
                                                                                                                                                                             17.1%; Score 47; DB 50.0%; Pred. No. 5.5; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.4%; Score 45; DB 50.0%; Pred. No. 33; ive 2; Mismatches
                                                     A;Gene: yqhB
C;Superfamily: hypothetical protein H10107
                                                                                                                                                                                                                                                                                                                                                                                                        396 VDTLGGWFLTQNIDAEPESA 415
                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                744 FDKYAGSTYDSALGLFLT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 FXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.29
                                                                                                                                                                                                                                                                                                                                                  62 VDSVXGVFLTQNXDXXSSXA
                                                                                                                                                                     Query Match
Best Local Similarity 50.0°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: ZK892.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: UU557
A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                 C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
T06602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conserved hypothetical protein yqhB - Bacillus subtilis
C;Species: Bacession: E6958
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Berter
C; Bron, S; Brouillatt, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M; Chc
A; Bhrlich, S.D; Emmerson, P.T.: Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulgar, D.; Fultz, C.; Fultian, M.; Fulta, Y.; Funa, S.; Galizzi, A.; Galler
A;Authors: Foulder, J; Lazarevic, V; Lee, S;M; Levine, A.; Luu, H; Masudel
Y; M; Ogawa, K.; Ogiwara, A.; Oddega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portectell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schlach, S.; Schroeter, R.; Socfione, F.; Sekiguchi, J; Sekowska, A.; Ostake, T.; Terpstra, P.; Terpstra, P.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Tanakoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, M.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:934377
A;Athere and Accession: E69588
A;Athere and A;At
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T32M21.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T44842
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De Wes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
Ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
Submitted to the Protein Sequence Database, March 2000
A;Reference number: 224487
A;Accession: T48452
A;Accession: T48452
A;Accession: T48452
A;Cross-references: EMBL:AL162875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:299116; GB:AL009126; NID:92634723; PIDN:CAB14406.1; PID:92634909
                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                          418 KVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLOGNRK 477
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                         1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXERXXFXXXXXFIXRMXXXQGXRX 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           931 KVDIDDETTRIWNLIMGKGDEKEGDEEKDKKKEKWWEEERRVFRGRADSFIARMHLVQG 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
C;Superfamily: Arabidopsis thaliana hypothetical protein F28A23.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: cultivar Columbia; BAC clone T32M21 C; Genetics:
                                                                                    Score 162; DB 2; I
Pred. No. 3.3e-19;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 FKQWKGSVVDSVVGVFLTQNTTDYLSSNAFMSVAAKFP 515
                                                                                                                                                                                                                                                                                                                                                                                                                              54 FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49.5;
Pred. No. 5;
                                                                                    Query Match 58.9%;
Best Local Similarity 43.9%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 167/1; 874/1
A;Note: T32M21.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-442 <KUN>
```

Matches

õ g

ö

Gaps

ö

ö

Gaps

ö

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

2002, 19:24:14 ; Search time 5.88235 Seconds (without alignments) 1470.857 Million cell updates/sec 8 November Run on:

US-09-840-743-71

Perfect score:

275 1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90 Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Query			SUMMAKLES	
No.	Score	Match	Length	DB	ID	Description
Н	163.5	9.	1207	7	D84781	hypothetical prote
۲.	162		917	7	T05430	
~•	49.5	8	1017	7	T48452	
4	47	17.1	442	~	E69958	Ω
Ŋ	47	7.	541	7	T28069	hypothetical prote
9	45		1131	7	F82875	_
7	43.5		327	7	T06602	
8	43.5	•	738	~	F96701	
6	43	•	217	7	C96748	O)
10	43	15.6	294	7	G83962	hypothetical prote
11	43	•	434	7	AH1353	
12	43		434	7	AI1723	_
13	43	15.6	565	7	T29718	hypothetical prote
14	43		832	7	H72278	Si
2	42		432	7	AE2799	HlyD family secret
9	42		437	~	G97578	probable periplasm
13	42		898	7	G82193	aminopeptidase N V
8	4	15.3	894	7	T01385	probable phosphopr
61	41.5	•	723	7	T30094	etical p
20	41	•	108	٦	WRBP69	protei
71	41	•	108	٦	WRBP13	protein
22	41	٠	108	7	JN0031	orotein
33	41	14.9	252	7	D81052	ansfera
24	41	14.9	253	~	G69199	endonuclease III-r
25	41	-	260	7	H69874	conserved hypothet
9	41	14.9	280	7	D84968	hypothetical prote
7	41	14.9	319	~	3	hypothetical prote
8	41	14.9	444	7	69	Ē
63	41	14.9	638	7	/	hypothetical profe

myosin IC - slime	RNA polymerase bet	probable lectin pr	gellan lyase (EC 4	preprotein translo	conserved hypothet	hypothetical prote	spou rRNA methylas	probable sugar ABC	citrate (si)-synth	citrate synthase,	glucan 1,4-alpha-g	hypothetical prote	probable heterochr	WD-40 repeat prote	hypothetical prote
T30578	S73652	T40912	T00047	E95237	F98101	B72776	G87396	AG0404	S41563	T49379	T49633	T23238	T37916	AC2239	T00637
~	7	~	7	7	7	7	~	~	7	~	7	~	7	7	7
1181	1391	312	2475	66	66	128	263	329	469	469	748	967	096	1526	1922
14.9	14.9	14.7	14.7	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5
41	41	40.5	40.5	40	40	40	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1

D84/81	
nypounctical protein Argistate   Imported   - Arabidopsis thallana	
C.Species: Atabidopsis chailana (Mouse-ear cress) C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001	
C; Accession: D84781	
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y	С.У
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon	lon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente	nter
Nature 402, 761-768, 1999	
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	
A; Reference number: A84420; MUID:20083487; PMID:10617197	
A; Accession: D84781	
A;Status: preliminary	
A; Molecule type: DNA	
A; Residues: 1-1207 <sto></sto>	
A; Cross-references: GB: AE002093; NID: 94581149; PIDN: AAD24633.1; GSPDB: GN00139	
C;Genetics:	
A;Gene: At2q36490	
A;Map position: 2	
Query Match 59.5%; Score 163.5; DB 2; Length 1207;	
Best Local Similarity 43.4%; Pred. No. 2.5e-19;	
Matches 43; Conservative 0; Mismatches 47; Indels 9; Gaps 2;	
OU I KUYXNAYWAYKAKAKIYYXXNAYWYYXYYYBBYYBBYYBTYBBYYRANANANA 60	

500 KVDLDDETDRVWKLLLENINSEGVDGSDEQKAKWWEEERNVFRGRADSFIARMHLVQGDR 559 g qq δλ

RESULT 2

hypothetical protein F28A23.180 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 23.Apr.1999 #sequence_revision 23.Apr.1999 #text_change 24.Nov-1999
C; Accession: T05430
R; Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A. Reference number: 215415
A; Reference number: 215415
A; Reference number: 215415
A; Residues: 1-917 < CBEV>
A; Residues: 1-917 < CBEV>
A; Cross-references: EMBL:AL021961

A; Experimental source: cultivar Columbia; BAC clone F28A23 C; Genetics:

A;Map position: 4 A;Introns: 41/3; 70/3; 88/1; 118/1; 321/1; 367/1; 474/1; 504/2; 624/3; 655/2; 667/3; A;Note: F28A23.180

```
The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
    it are useful for selecting probes and primers for detecting genes in L.
    concluded by the genome sequence of the present sequence is a protein
    concoded by the genome sequence are useful for raising specific
    antibodies, identification of L. monocytogenes and related organisms, and
    for biosynthesis and biodegradation, especially biosynthesis of vitamin
    Concompounds that regulate gene expression and cell replication
    concoded by the genome sequence are useful for varieties of vitamin
    controlled to monocytogenes related diseases. In addition, the genome
    concounts of the treatment or prevention of infections by L.
    concince and proteins for the treatment or prevention of infections by L.
    concince and related organisms.
    concounts for the treatment or prevention of infections by L.
    concounts the sequence data for this patent did not form part of the printed
    concounts the concounts of the printed organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dussurget C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Varquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.4%; Score 72; DB 23; 25.2%; Pred. No. 0.0017; ive 8; Mismatches 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID No 720; 192pp; French.
                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes protein #719.
                                                                                ABB48015 standard; Protein; 219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000; 2000FR-0004629.
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200177335-A2.
                                                                                                                                                                                                                                                  05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2001
                                                                                                                                                                 ABB48015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
RESULT 15
ABB48015
```

3;

18;

51; Indels

Best_Local Similarity 25.2 Matches 26; Conservative

96

ò qq

GXGLKSXECVRLLXLXXXAFPVDTNVGRLXVRXGXVPLXPLPXXXQXHXLXXYPXXXXQ 155

156 KXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198

```
Search completed: November 8, 2002, 19:25:57
Job time : 38.7026 secs
              g
```

œ

```
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centifisade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143,
useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein into a cell results in adelay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylatycosine glycosylases and regulates
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                            DB 23; Length 166;
5.4e-08;
thes 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lecompte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thierry JC, Prieur D, Dietrich J, I
Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                              Score 98; DB 2
Pred. No. 5.4e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   178 ITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative P. abyssi endonuclease III #1
                                                                                                                                                                                                                                          sequence represents a DMT-like protein
                                                                                                                                                                                                                                                                                                                                                                                                        2 ITFGK-VFCTKRQPNCNACPM-RSECKHFASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 851; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB96207 standard; Protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                              14.1%;
65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99FR-0005034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99FR-0005034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                            Query Match 14.1
Best Local Similarity 65.6
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-126236/14
                                                                                                                                                                                                                                                                            166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FR2792651-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB96207;
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB96207
                                                                                                                                                                                                                                                                                                                                                                                                        ø)
                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

223 AA;

Sequence

```
4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90221) and related proteins (ABB5300-ABB55621). The nucleic acid sequence, is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus laction related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The production helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent W0200177334 (published 18-077-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                           LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                        119 LIKLPGIGRKCANIVLAYGFGIPAIPVDTHVYRISRRLGLAPWDASPEEVEERL---- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KXXLLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXX 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 YPXXXXXQKX----LWPRLCKLX-QXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                          Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 218;
                                                                                                                                         ----KELIPR-----EEMIY-VNHAMVDHGK-SVCRPIKPRCDECPL 208
                              50; Indels
                                                                                                                       151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Indels
 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ehrlich SD;
DB 22;
7.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 74; DB 23;
Pred. No. 0.00077;
9; Mismatches 49;
; Score 86; DB
; Pred. No. 7.6e
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID No 1089; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorokine A, Renault P,
                                                                                                                                                                                                                                 ABB54387 standard; Protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                             Lactococcus lactis protein nth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 10.7%;
1 Similarity 25.9%;
30; Conservative
12.4%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lactis and related species
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis IL1403
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-043418/06.
              L Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      FR2807446-Al.
                                                                                                                                                                                                                                                                                             16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bolotine A,
                                                                                                                                                                                                                                                              ABB54387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112
                              Matches
                                                           91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                     ABB54387
                                                                                        qq
                                                                                                                                                      qq
                                                                                                                                                                                                                                                              q
                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pp
```

```
WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2002
                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                            AAU72746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays.
                                                                                                          Sequence
                                                                                                                                  Query Match
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                     AAU72746
                                                                                                                                                                                                                                                                                                                                                                                                  25000000x3
                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement encoding a polymetrical control of a sequence at least 40% identical to DWT (DEWETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polymucleotide or comprising a heterologous polymucleotide under the control of a promoter at least 70% identical to DWT 5 flanking sequence or an 5 untranslated encoding a more properties of a ranspenic plant comprising an exception of DWT. It is protein and a transpenic plant comprising a modulating transcription. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the cassette into a host cell with modulated transcription, where the cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following protein in a plant results in a delay in flowering the protein into a cell results in modulation of methylation of
                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                           IXXRGXXXXLXXRIXXXXXXXXXXXXFLXXXVXXXXGXIDLEWLRXXXXXXXXXXLLXXXG
                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                           Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                         Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tatarinova TV;
                                                                                                       Score 141; DB 23;
Pred. No. 2.8e-15;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 86; 109pp; English.
                                                                                                                                                                                                                                                                                                        AAU72747 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hannon M,
                                                                                                                                                                                                            97 XGLKSXECVRLLXLXXXAFPVD 118
                                                                                                                                                                                                                                      124 LGLKSVECVRLLTLHHLAFPVD 145
                                                                                                         20.3%;
45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                     Local Similarity 45.1 les 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-055307/07
                                                                                                                                                                                                                                                                                                                                                                                   Corn DMT3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200180626-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fischer RL,
                                                                                                                                                                                                                                                                                                                                                          26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                 AAU72747;
                                                                                Sequence
                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
                                                                                                                                                           37
                                                                                                                                  Matches
                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                             AAU72747
  22222×8
                                                                                                                                                                                  qq
                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                         0
```

```
3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMFTER, previously known as ATROPOS (ATR)) Domain A, Bor or C or their combinations. Also included are an expression cassette comprising the polymucleotide or comprising a heterologous polymucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polymucleotide encoding a DMT-like protein and a transgenic plant comprising a polymucleotide encoding a DMT-like protein. The expression cassette is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sedneuce
chromosomal DNA in the cell, reduction of expression of the protein in plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylovytosine glycosylases and regulates transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 GXIDLEWLRXXXXXXXXXXXLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 PLXPLPXXXQXHXLXXYPXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKX-XFCT--- 187
                                                                                                                                                                                                                                                                                                                                                                                                        24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 GKICLEYLRELSVDEVKKELSRFKGIGPKTVACVLMFYLQKDDFPVDTHVLRITKAMGWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             development comprising a domains A, B or C -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                       Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                       , DB 23;
4.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                       Score 106;
                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide that control planting a specific homology to DEMETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 85; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU72746 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 PATASREKAYIHLNN------
                                                                                                                                                                                                                                                                                                                                       15.3%; 27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 GSDKRKSSNSACPLAGYC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 ---KXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-055307/07
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                         276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corn DMT2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS96697
```

```
complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B complement encoding a polypeptide having a sequence at least 40% or C or their comprising the polynucleotide or comprising a heterologues polynucleotide under the control of a promoter at least 70% identical to DMT 3. flanking sequence, DMT 3. flanking sequence or an 5. untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising at region of DMT-like protein. The expression cassette is useful for modulating transcription. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following blological activities, which include enhanced expression of the chaptorin into a cell results in modulation of methylation of the protein into a cell results in modulation of methylation of chaptor results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene.

The polynucleotide is useful for detecting a nucleic acid in a sample.

The DEMETER is related to 5-methylcytosine glycosylases and regulates
   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide sequence or their
                                                                                                                      97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156
       Gaps
                                                                    IXXRGXXXXLXXRIXXXXXXXXXXXXXXXVXXXGXIDLEWLRXXXXXXXXXXXXC 96
   35;
                                                                                                                                                                                                                                                                      HILLI HILL I HILLI HILLI
                                                                                                                                                                                                                                                                                                                                                              157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                            Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tatarinova TV;
56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamuro JK,
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean DMT protein related sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 95; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU72761 standard; Protein; 179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hannon M,
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2002 (first entry)
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fischer RL, Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS96711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-2001
82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU72761;
                                                                    37
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU72761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XX
DE
                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                            g
                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT S' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide encoding a DM-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by saxual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising a sequence or C
                                                                                                                                                                   129 GXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTK 188
                                                                                                                                  Gaps
                                                                                                                                                                                         2 GWVPLQPLPESLQLHLLELYPVLESIQKYLWPRLCKLDQETLYELHYQMITFGK-VFCTK 60
                                                                                                                              2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tatarinova TV;
                                                                                          Score 255; DB 23; Length 179;
Pred. No. 2.5e-34;
0; Mismatches 28; Indels
transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide that control plant development com
having a specific homology to DEMETER domains A,B or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 87; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                AAU72749 standard; Protein; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hannon M,
                                                                                                                                                                                                                                                189 XXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                    61 SKPNCNACPM-RAECRHFASA 80
                                                                                            36.8%;
63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-2000; 2000US-0553690
                                                                    Query Match
Best Local Similarity 65.v.
8.conservative
"... 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-055307/07.
N-PSDB; AAS96699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wheat DMT2 protein.
                                                         179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum sp.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAU72749;
                                                           Sequence
                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                       S S X S
                                                                                                                                                                         δ
                                                                                                                                                                                                                                                ò
```

S

ò

```
37
                                                                                                                                                                                                  6
                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                 ABB92260
    0000x8
                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                  ò
                                                                                                                                                 δ
                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% complement encoding a polypeptide having a sequence at least 40% condentical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or condential comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5. flanking sequence, DMT 3. flanking sequence or an 5. untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a crossin cassette is polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cross and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following bological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a handle endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene.
                             3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                         156
                                                                                                                     37 IXXRGXXXXLXXXXXXXXXXXXXXXXXXXXXX 95
                               Gaps
                                                                                                         XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK
                            12;
                                                                                                                                                                        942 YLWPRLCKLDQKTLYELHYHMITFGR-VFCTKVKPNCNACPM-KAECRHYSSA 992
                                                                                                                                                                                                                                                                                                                                                       Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
 Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tatarinova TV;
                                                                                                                                                          157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA
                            Indels
                             62;
  DB 23;
 Score 432; DB 23;
Pred. No. 4.1e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okamuro JK,
                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 89; 109pp; English.
                                                                                                                                                                                                                                                 AAU72753 standard; Protein; 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hannon M,
62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2001; 2001WO-US13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                      (first entry)
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-055307/07.
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS96703
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200180626-A1
                                                                                                                                                                                                                                                                                                                               Soybean DMT2
                                                                                                                                                                                                                                                                                                     26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-2001
                           96;
 Query Match
                Best Local
                                                                                                        97
                           Matches
                                                                                                                                                                                                                                    AAU72753
                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                              g
                                                                             g
                                                                                                                                                          ò
```

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
     samble.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                        109 IKERGMNNMLAERI------QSFLNLLVDKHGGIDLEWLRDVPPDQAKEFLLSIRG 158
                                                                                                                                                                                                                                                                                                                                                                                                               XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 LGLKSVECVRLLTLHHLAFPVDTNVGRIAVRLGWVPLQPLPESLQLHLLELYPVLESIQK 218
                                                                                                                                                                                                                                                                                                     Identifying plant target proteins for herbicidally active compounds,
The polynucleotide is useful for detecting a nucleic acid in a san DEMETER is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present
                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23; Length 1309;
                                                                                                                                                                                           Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 1471; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                             57;
                                                                                                                                                                                        Score 373.5; DB 2
Pred. No. 4.6e-54;
); Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 335.5; DB 2: Pred. No. 6.5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbicidally active_polypeptide SEQ ID NO 1471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 YLWPRLCKLDQRTLYELHYQLITFGK-VFCTK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herbicidal; plant; agriculture; herbicide
                                                                                 sequence represents a DMT-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB92260 standard; Protein; 1309 AA
                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                     53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weidler
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                      251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-2002
                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organisms
                                                                                                                                      Sequence
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB92260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                          Local
```

97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156

q

```
1554 YLWPRLCKLDQRTLYELHYQMITFGK-VFCTKSKPNCNACPM-RAECKHFASA 1604
g
```

```
The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATRODOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic comprising a cassette is polynucleotide encoding a DMT-like protein. The expression cassette is polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following brotein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of the protein in an Arabidopsis leaf results in expression of the MEDRA gene content in an Arabidopsis leaf results in expression of the MEDRA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide to 5-methylcytosine glycosylases and requlates transcription of target genes by demethylation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                                                                                                         Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 432; DB 23;
Pred. No. 8.4e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 88; 109pp; English.
                                  AAU72752 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%;
56.6%;
                                                                                                                                                                                                                                                                                                                                                                                      23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-0553690
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                    Soybean DMT1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fischer RL, Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS96702
                                                                                                                                                                                                                                                                                                           WO200180626-A1
                                                                                                             26-FEB-2002
                                                                                                                                                                                                                                                                        Glycine max.
                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001
                                                                       AAU72752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
RESULT
```

```
The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide concoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynuclectide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                     Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 71; 109pp; English.
                                                                                                                                             AAU72739 standard; Protein; 1332 AA.
                                                                                                                                                                                                                                                                     Arabidopsis DMT3 (1DMT3) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis Thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS96693
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200180626-A1.
                                                                                                                                                                                                                            26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2001
                                                                                                                                                                                       AAU72739;
                                                                                                  RESULT 6
                                                                                                                                                                                       οy
```

æ

sequence represents a DMT-like protein.

3;

12;

63; Indels

0; Mismatches

98; Conservative

Matches

ð 8

Best Local Similarity

1332 AA;

Sednence

us-09-840-743-72.rag

AAU72743;

```
complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or or their compinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous cor C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence or an 5' untranslated region of DMT. The protein and a transgenic plant comprises in introducing concoding a DMT-like protein. The expression cassette is polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in adelay in flowering time of the protein in a plant results in adelay in flowering time protein in a plant results in modulation of expression of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and requlates the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or \mathtt{C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 54-55; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi Y, Hannon M,
                                                                                                                                                                                        23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                    21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS96686, AAS96689.
                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-055307/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1729 AA;
WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fischer RL,
                                                                                                01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
```

```
ë.
                                                                                                  1214 DSIDYEAIRRASISEISEAIKERGMNNMLAVRI------KDFLERIVKDHGGIDLE 1263
                                                                                                                                                                                                                       78 WLRXXXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                    138 XXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACP 197
                                                                  62.5%; Score 433; DB 23; Length 1729;
51.0%; Pred. No. 3.7e-63;
ive 0; Mismatches 82; Indels 12
                                 98; Conservative
                                                                                                                                                                                                                                                                                                      1383 M-RGECRHFASA 1393
                                                                                                                                                                                                                                                                      MXXXECXXXXSA 209
               Best Local Similarity
 Query Match
                               Matches
                                                                                                                                 ò
                                                                                                                                                                 g
                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                      δ
```

AAU72743 standard; Protein; 1952 AA.

RESULT 4 AAU72743

ä,

```
The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a prometer at least 70% identical to DMT 5′ flanking sequence, DMT 3′ flanking sequence or an 5′ untranslated region of DMT, a host cell comprising an exogenous polynucleotide concoding a DMT-like protein and a transgent of pant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual.

The protein is capable of exhibiting at least one of the following the protein in a plant results in adelay in flowering time, introduction of the protein into a cell results in adelay in flowering time, introduction of the protein in an Arabidopsis leaf results in modulation of methylation of protein in an Arabidopsis leaf results in expression of the MEDRA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. Sequence represents a DMT-like protein. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1444 IRERGMNNMLAERI------KDFLNRLVRDHGSIDLEWLRYVDSDKAKDYLLSIRG 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 IXXRGXXXXLXXRIXXXXXXXXXXXXXXVXXXXXXXXIDLEWLRXXXXXXXXXXXXC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 12;
                                                                                                         Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1952;
                                                                                                                                                                                                                                                                                                                                                                                                         Okamuro JK, Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 433; DB 23;
Pred. No. 4.2e-63;
0; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 79-80; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.5%;
55.5%;
                                                                                                                                                                                                                                                                                            23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000US-0553690.
                                  26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                        Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI: 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1952 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                      Rice DMT1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS96695
                                                                                                                                                                                                                      40200180626-A1.
                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Ma.
Local St.
96;
                                                                                                                                                                                                                                                          01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                         Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
21-APR-2000; 2000US-0553690.
                               (REGC ) UNIV CALIFORNIA.
                                                            Fischer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU72736
    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                     The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at lesst 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a prometer at least 70% identical to DMTs flanking sequence, DMTs flanking sequence or an 5° untranslated region of DMT, a host cell comprising an exceptions polynucleotide encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein into a cell results in modulation of methylation of the protein into a cell results in modulation of methylation of the protein into a cell results in modulated expression of the protein in a hanneed endosperm development and expressing of the component and expression of the DEMETER is related to 5-methylcytosine glycosylasses and regulates and requiates and requiates and represent and expression of the protein in a nample of the content of the protein of target genes by demethylation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  874 EKTRSTMDTVDWKAIRAADVKEVAETIKSRGMNHKLAERIQYLTLNMKIMQGFLDRLVND 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 XGXIDLEWLRXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGX 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          934 HGSIDLEWLRDVPPDKAKEYLLSFNGLGLKSVECVRLLTLHHLAFPVDTNVGRIAVRLGW 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 VPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXX 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 440; DB 23; Length 1413;
Pred. No. 2e-64;
0; Mismatches 98; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a DMT-like protein
                Disclosure; Page 67; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU72741 standard; Protein; 1114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis DMT4 (1DMT4) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1053 PNCNACPM-KGECRHFASA 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 63.5%;
Local Similarity 49.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 PNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis Thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                          1413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU72741;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   С
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
The invention features to an isolated polymeracture at least 40% identical to DMT (DEMTER, previously known as ATROPOS (ATR)) Domain A, B complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMTER, previously known as ATROPOS (ATR)) Domain A, B cr C or their compinations. Also included are an expression cassette comprising the polymeractice or comprising a heterologues polymeractic demonstrating sequence, DMT 3. flanking sequence or an 5. untranslated region of DMT, a host cell comprising an exogenous polymeracing a crossing a DMT-like protein and a transgenic plant comprises introducing encoding a DMT-like protein. The expression cassette is polymeractic encoding a DMT-like protein. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual tross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polymeracticities useful for detecting a nucleic acid in a sample. The polymeracticities a DMT-like protein. The present reputates
                                                                                                                                                                                                    New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        595 IKKRGQFRILSERI------LKFLNDEVNQNGNIDLEWLRNAPSHLVKRYLLEIEG 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          705 YLWPRICKLPQETLYELHYQMITFGK-VFCTKTIPNCNACPM-KSECKYFASA 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.5%; Score 433; DB 23; Length 1114;
Best Local Similarity 55.5%; Pred. No. 2.3e-63;
Matches 96; Conservative 0; Mismatches 65; Indels 12;
Tatarinova TV;
Okamuro JK,
                                                                                                                                                                                                                                                                                                                              Disclosure; Page 75; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU72736 standard; Protein; 1729
Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis Demeter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis Thaliana.
Choi Y,
                                                                              WPI; 2002-055307/07.
N-PSDB; AAS96694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU72736;
```

3;

us-09-840-743-72.rag

```
New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU72737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
57
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU72737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis Demete
Rice DMT1 protein.
Soybean DMT1 prote
Arabidopsis DMT3 (
Soybean DMT2 prote
Herbicidally activ
Soybean DMT protei
Wheat DMT2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis DMT2
Arabidopsis DMT4
                                                                                                          8, 2002, 19:24:08; Search time 35.7026 Seconds (without alignments) 858.415 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS2/gcgdata/geneseqy/geneseqp-emb1_AA1981.DAT:*
| SIDS2/gcgdata/geneseqy-emb1_AA1981.DAT:*
| SIDS2/gcgdata/geneseqy/geneseqp-emb1_AA1983.DAT:*
| SIDS2/gcgdata/geneseqy/geneseqp-emb1_AA1984.DAT:*
| SIDS2/gcgdata/geneseqy/geneseqp-emb1_AA1985.DAT:*
| SIDS2/gcgdata/geneseqy-emb2_AA1985.DAT:*
| SIDS2/gcgdata/geneseqy-emeseqp-emb1_AA1986.DAT:*
| SIDS2/gcgdata/geneseqy-embseqp-emb1_AA1989.DAT:*
| SIDS2/gcgdata/geneseqy-embseqp-emb1_AA1989.DAT:*
| SIDS2/gcgdata/geneseqy-embseqp-emb1_AA1989.DAT:*
| SIDS2/gcgdata/geneseqy-embseqp-emb1_AA1989.DAT:*
| SIDS2/gcgdata/geneseqy-embseqp-emb1_AA1989.DAT:*
                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991_DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992_DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993_DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994_DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995_DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995_DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996_DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996_DAT:
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU72741
AAU72736
AAU72743
AAU72752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU72739
AAU72753
ABB92260
AAU72761
AAU72749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU72737
                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΩI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                                                         US-09-840-743-72
693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1413
1114
1729
1952
298
1332
251
1309
179
                                                                                                             November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433
433
432
432
373.5
335.5
255
141
                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                         •
                                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
```

```
Human mutant cysta
Human cystatin D (
                                                                                                                                                                                                  Human cystatin D p
Human cystatin D p
Human cystatin D p
Arabidopsis thalia
Arabidopsis thalia
Leishmania antigen
Leishmania antigen
                                       S. epidermidis ope
S. epidermidis ope
Staphylococcus epi
                                                              Drosophila melanog
Drosophila melanog
Amino acid of the
                                                                                     Escherichia coli (
Human cystatin D.
Human wild-type cy
               Putative P. abyssi
Lactococcus lactis
                                                                                                                                                                                                                                                         Leishmania antigen
Leishmania antigen
Leishmania antigen
                                Listeria monocytog
                                                                                                                     AAY81172
AAY81173
AAY81174
                                                                                                                                                                                    AAE11210
AAE04437
                                                                                                                                            AAY81175
AAY81176
                                                                                                                                                                                                    AAE02408
AAO15149
                                                                                                                                                                                                                    AAY81178
AAG12675
                                                                                                                                                            AAY81177
AAY81181
                                                                                             AAB37443
                                                                                                                                                                            AAY81182
                                                                                                              AAY81171
106
98
74
72
72
68
68
67
61
61
```

## ALIGNMENTS

```
Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamuro JK,
AAU72737 standard; Protein; 1413 AA.
                                                                                                                                         Arabidopsis DMT2 (1DMT2) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hannon
                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-2001; 2001WO-US13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-0553690
                                                                                          26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fischer RL, Choi Y,
                                                                                                                                                                                                                                                                                     Arabidopsis Thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-055307/07.
N-PSDB; AAS96692.
                                                                                                                                                                                                                                                                                                                                   WO200180626-A1.
```

```
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 ECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 ECV-----GIAVDTHVHRISNRLGWIK-TSTPEKTQKALEILLP-----KSEW--- 172
                    --- 74
                                                                                                                                                                                              Sequence 36, Application US/08808550
Patent No. 5871992
ENBEAL INFORMATION:
APPLICANT: Teebor, George W.
APPLICANT: Hilbert, Timochy P.
TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                         155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                  ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,550
FILING DATE: 26-FEB-1997
CLASSIFICATION: 435
38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.0%; Score 48.5; Di 23.4%; Pred. No. 5.9; vative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 CKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 -----QPINHLLVGFGQMQ-CQPVRPKCGTC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1049-1-001 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-808-550-39
; Sequence 39, Application US/08808550
; Patent No. 5871992
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 1049-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.0%
Best Local Similarity 23.4%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                         US-08-808-550-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us-08-808-550-36
                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                  g
                                                                                             g
```

```
103 ECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXXQKXLWPRL 162
         APPLICANT: Hilbert, Timothy P.

TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF

WOMBER OF SEQUENCES: 42

CORRESPONDENCES: 42

ADDRESSEE: David A. Jackson, Esq.

STREET: 111 Hackensack Ave, Continental Plaza, 4th

STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 48.5; DB 2; Length 259; llarity 23.4%; Pred. No. 7.4; Conservative 7; Mismatches 38; Indels 2'
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,550 FILING DATE: 26-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-001 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 CKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8, 2002, 19:29:16
                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
George W.
                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO FRAGMENT TYPE: N-termin ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November
Job time: 15.1536 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 22; Conserva
                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
Teebor,
                                                                                                                                                                                                                                                          07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-808-550-39
                                                                                                                                                                   STREET:
CITY: Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
```

5

S

ä

```
96 GXGLKSXE-CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                          51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 GXGLKSXE-CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                Score 55.5; DB 4; Length 320; Pred. No. 0.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55.5; DB 4; Length 320;
Pred. No. 0.7;
7; Mismatches 30; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                  155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/No.^^
                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55, Application US/09022765; Patent No. 6375955; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MC-SOPTIVE SYSTEM: PC-DOS/MC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%;
19.3%;
                                                                                                                                                                                                              Query Match 8.0%;
Best Local Similarity 19.3%;
Matches 21; Conservative 7
    (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
                     TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 320 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.0°
Best Local Similarity 19.3°
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                        ; MOLECULE TYPE: protein US-09-022-765-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washing
  TELEPHONE:
                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-022-765-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 GXGLKSXE-CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Webb, John R.
APPLICANT: Webb, John R.
APPLICANT: Stellon, Davin C.
APPLICANT: SKELLY, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.0%; Score 55.5; DB 4; Length 320; 19.3%; Pred. No. 0.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/183,861 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: SEED and BERRY LLP
F: 6300 Columbia Center, 701 Fifth Avenue
Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/02,765
FILING DAME: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE GLARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09022765
Patent No. 6375955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-FEB-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 320 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.0
Best Local Similarity 19.3
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-183-861-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITA.
STATE: Was...
COUNTRY: USA
TO 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-022-765-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
CITY: Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
```

qq δλ

RESULT 9

g

```
96 GXGLKSXE-CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 55, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES: 87
CORRESPONDENCE SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                 APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55.5; DB 4; Length 320;
Pred. No. 0.7;
7; Mismatches 30; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYEE Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
                                                                                                                       E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.0%;
Best Local Similarity 19.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-183-861-22
  Webb, John R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                            98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
                                                                                                                                                                     Seattle
                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-183-861-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match

8.3%; Score 57.5; DB 4;
Best Local Similarity 41.7%; Pred. No. 0.14;
Matches 10; Conservative 4; Mismatches 9;
                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                          APPLICANT: Gentz, Reiner L.
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TYPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: Human Cystatin E
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DCKET NUMBER: PF202P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301 309 8504
TELEFAX: 301 309 8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,376
                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/744,138
FILING DATE: 05-NOV-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,030
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; INDIVIDUAL ISOLATE: Cystatin D US-09-241-376-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 YYENVKFGRTT-CTKSQPNLDNCP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
84 YYFNVKFGRTT-CTKSQPNLDNCP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G. APPLICANT: Campos-Neto, Antonio
                                                                                                   Sequence 4, Application US/09241376
Patent No. 6300477
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 301 309 8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                       STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-183-861-22
                                                                               US-09-241-376-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
```

ò q

ë

us-09-840-743-72.rai

```
142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-617-302-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-431-480-7
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                3;
TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA TITLE OF INVENTION: MISMATCHES
                                                                                                                                                                                                                                                                                                                                                                                     96 GXGLKSXECVRLLXLXXXAFPV-DTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                          116 GVGRSTAGAILSLSLGKH-FPILDGNVKRVLAR-------CYAVSGWPGKKEV 160
                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                        DB 4; Length 350;
                                                                                                                                                                                                                                                                                                                                                53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,138
                                                                                                                                                                                                                                                                                                      Score 59; DB 4
Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                   FILE REFERENCE: IL-10284
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Wosen, Craig A.
TITLE OF INVENTION: Human Cystatin
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36,373
PF202P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; INDIVIDUAL ISOLATE: Cystatin D
US-08-744-138-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08744138
Patent No. 6011012
GENERAL INFORMATION:
APPLICANT: Gentz, Reiner L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BROACES, A. AnderS
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF20
TELECOMUNICATION INFORMATION:
TELEPHONE: 301 309 8504
TELEPHONE: 301 309 8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                      Query Match 8.5%;
Best Local Similarity 20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                             21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                     TYPE: PRT
; ORGANISM: Escherichia coli
US-09-650-855-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 9410 Key
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
.US-08-744-138-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
```

```
ή
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Holloway, James L.
APPLICANT: Feldhaus, Andrew
TITLE OF INVENTION:
FILE REFERENCE: 98-72 C1
CURRENT APPLICATION NUMBER: US/09/617,302
CURRENT PILING DATE: 2000-07-17
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Holloway, James L.
APPLICANT: Feldhaus, Andrew
APPLICANT: Feldhaus, Andrew
TTTLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
FILE REFERENCE: 98-72
CURRENT APPLICATION NUMBER: US/09/431,480
CURRENT PILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: 60/109,217
EARLIER APPLICATION NUMBER: 60/156,382
EARLIER FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
8.3%; Score 57.5; DB 3; Length 142; 41.7%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.3%; Score 57.5; DB 4; Length 142; 41.7%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%; Score 57.5; DB 4; Length 142;
11.7%; Pred. No. 0.14;
ive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                 84 YYFNVKFGRTT-CTKSQPNLDNCP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 HYXXITEGKXXECTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                      Sequence 7, Application US/09431480 Patent No. 6235708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09617302
Patent No. 6245529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.3%;
Best Local Similarity 41.7%;
Matches 10; Conservative
                      Best Local Similarity 41.79
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.3%
Best Local Similarity 41.7%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-617-302-7
```

~

```
RESULT 5
US-09-650-855-37
Sequence 37, Application US/09650855; Patent No. 6365355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/09651656 Patent No. 6340566
                    34,344
                                                                                                                            INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 350 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Escherichia coli
US-09-651-656-37
                                                                                           TELEFAX: 610-270-4026
                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-813-574-9
Han, William T
                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-651-656-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 37
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΟŻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 LLXXXGXGLKSXECVRLLXLXXXAAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 LVKLPGVGRKTANVVVSVAFGVPAIAVDTHVERVSKRLGICRWKDSVLEVEKTLMRKVP- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.2%; Score 64; DB 2; Length 209; Best Local Similarity 23.1%; Pred. No. 0.02; Matches 25; Conservative 10; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 -----KEDWS------VTHHRLIFFGR-YHCKAQSPRCAECPL 201
                                                                                       COMPOUR: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILICATION NUMBER: US/08/808,550
FILING DATE: 26-FEB-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08813574; Sequence 9, Application US/08813574; Patent No. 6013473; GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei; TITLE OF INVENTION: Human MutY NUMBER OF SEQUENCES: 18; CORRESPONDENCE ADDRESS: ADDRESSE: Smithkline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STREET: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,574
                                                                                                                                                                                                                                                                                           1049-1-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013,132
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Bacillus subtilis US-08-808-550-31
                                                                                                                                                                                                                                                                                     REFERENCE DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                          TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                              209 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-813-574-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
```

```
÷,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERNORE NATIONAL LABORATORY
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: MCUTHEN-MALONEY, SANDRA
APPLICANT: MCUTHEN-MALONEY, SANDRA
APPLICANT: MCUTHEN-MALONEY, SANDRA
APPLICANT: MCUTHEN-MALONEY, SANDRA
APPLICANT: MCUTHEN-BINGE INFORMATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: DOLIMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
FILE REFERENCE: IL-10689
CURRENT FILING DATE: 2000-08-29
PRIOR RAPLICATION NUMBER: 06/192,764
PRIOR PALLING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 GVGRSTAGAILSLSLGKH-FPILDGNVKRVLAR--------CYAVSGWPGKKEV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 GXGLKSXECVRLLXLXXXAFPV-DTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GXGLKSXECVRLLXLXXXAFPV-DTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 ENKLWSLSEQVTPAVGVERFNQAMMDLGAMICTRSKPKCSLCPL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.5%; Score 59; DB 4;
Best Local Similarity 20.2%; Pred. No. 0.21;
Matches 21; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.5%; Score 59; DB 3; Best Local Similarity 20.2%; Pred. No. 0.21; Matches 21; Conservative 14; Mismatches
REFERENCE/DOCKET NUMBER: ATG50002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
```

_

us-09-840-743-72.rai

```
US-08-795-445A-52
US-08-795-447A-52
US-08-795-446B-52
US-08-795-446B-52
US-08-26-139
US-08-26-139
US-09-150-86A-6
US-09-150-86A-6
US-08-012-269A-2
US-08-012-269A-2
US-08-13-574-2
US-08-13-574-2
US-08-13-574-2
US-08-13-574-2
US-09-241-376-7
US-09-241-376-7
US-09-241-376-7
US-09-241-376-7
US-09-619-062-2
US-09-619-062-2
US-09-619-062-2
US-09-619-062-2
US-09-619-062-2
191
191
191
191
191
191
191
141
141
111
2052
2052
2052
 2002, 19:24:15; Search time 13.1536 Seconds (without alignments) 514.481 Million cell updates/sec
                                                                  5.1.3
Compugen Ltd.
                                                                                                              262574 segs, 29422922 residues
       version
- 2002
                              sw model
                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
       GenCore
Copyright (c) 1993
                              protein search, using
                                           8
                                           November
```

Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 139, Appl Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 17, Appli Sequence 17, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli

## US-09-134-001C-3225

Sequence 3225, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PEDICATION NUMBER: US 60/055,779

; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3225

Gaps 20; Length 224; 48; Indels Score 67; DB 4; Pred. No. 0.007; 13; Mismatches 9.78; 23; Conservative Best_Local Similarity Matches 23; Conservat Query Match

96 GXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXYLPXXXQXHXLXXYPXXXXXQ 155

ŏ

3;

156 KXLWPRLCKLXQXTLY-ELHYXXITFGKXXFCTKXXPNCNACPM 198 Db

RESULT 2 US-08-808-550-31 164 à g

Sequence 31, Application US/08808550
Patent No. 5871992
GENERAL INCOMATION:
GENERAL INCOMATION:
APPLICANT: Teachor, George W.
APPLICANT: Hilbert, Timothy P.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF NUMBER OF SEQUENCES: 4.2
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor

Hackensack

ALIGNMENTS

262574

Total number of hits satisfying chosen parameters:

Title: Perfect score: Sequence:

OM protein -Run on: Scoring table:

			•				
Minimum DB Maximum DB	sed	length: length:	2000000000	0000	0		
Post-processing	ssing	Minimum Maximum Listing	num Match num Match ng first		0% 100% 45 summaries		
Database :		Issue 1: /ce 2: /ce 3: /ce 4: /ce 5: /ce	ssued_Patents_AA:* /cgn2_6/ptodata/ /cgn2_6/ptodata/ /cgn2_6/ptodata/ /cgn2_6/ptodata/ /cgn2_6/ptodata/	otod otod otod otod otod otod	<pre>ued_Patents_AA:* /cgn2_6/ptodata/1/iaa/5A_COMB.pep:* /cgn2_6/ptodata/1/iaa/5B_COMB.pep:* /cgn2_6/ptodata/1/iaa/6A_COMB.pep:* /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*</pre>		
Pred. score and i	~ ິດ	No. is the numbe greater than or derived by anal	number of an or equal y analysis	equal	No. is the number of results predicted by chance to reater than or equal to the score of the result bein derived by analysis of the total score distribution	se to have a It being printed, oution.	
Result	Score	% Query Match ]	Length	DB	SUMMARIES	Description	
11, 10, 10, 10, 10, 10, 10, 10, 10, 10,	799 799 799 799 799 799 799 799 799 799	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	2026 33509 4202 33509 4422 5220 5220 5220 5220 5220 5220 5220	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	09-134-001C 08-808-550- 08-651-656- 09-651-656- 09-650-855- 09-613-376- 09-133-861- 09-133-861- 09-012-765- 09-022-765- 09-022-765- 09-032-765- 09-032-765- 09-03-38- 09-03-38- 09-03-38- 09-03-48- 09-03-48- 09-03-48- 09-03-431-480- 09-03-431-480- 09-03-431-480- 09-03-431-480- 09-03-431-480- 09-03-431-480- 09-03-431-480- 09-03-617-376- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-03-776- 09-	ण व व्यव्य ल व्यव्यव्यव्य	
	47.5	6.9 6.8	146 191	9 %	5432264-6 US-08-974-022-52	52,	

THIS PAGE BLANK (USPTO)

ολ

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09775932;
Patent No. US20020137671A1
GENERAL INFORMATION:
APPLICANT: University of British Columbia
TITLE OF INVENTION:
FILE REFERENCE: 58069
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 1999-08-05
PRIOR PLICATION NUMBER: 60/095,503
PRIOR PLICATION NUMBER: 60/095,503
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO. 6
LENTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                            OTHER INFORMATION: MAP TO ACO11301.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEBLIOO, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HERRT, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

US-09-864-761-35736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 10; Length 121;
Pred. No. 3.6;
6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.5%; Score 45; DB 10; Length 84; 50.0%; Pred. No. 2.4; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 RLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: : | |: : | |: | 49 RVLRARQQTVGGVNYFFDVEVGRTICTKSQPNLDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: November 8, 2002, 19:29:41 Job time: 8.14052 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 27.89
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 TKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-09-775-932-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 SQLAPNCTACPL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-775-932-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-X-
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                   Length 494;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-3

PRIOR FILING DATE: 2000-06-3

PRIOR FILING DATE: 2000-06-03

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-20

PRIOR PILING DATE: 200
                                                                                                                                                                                                                                                                                                            Score 45.5; DB 10;
Pred. No. 14;
6; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 CAQMLAMVSLPFYLQTVLGRSEVETGLL-LTPWP 351
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 468
LENGTH: 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35736, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                            Query Match 6.6%;
Best Local Similarity 32.4%;
Matches 11; Conservative
                                                                                                                                                                         TYPE: PRT; ORGANISM: Escherichia coli
US-09-741-669-468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-864-761-35736
```

ö

```
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE LOCATION: (438)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAID.
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PGT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR PLING DATE: 1099-03-08
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                    FILING DATE: (UNKNOWN)
FILING DATE: (UNKNOWN)
APPLICATION NUMBER: US/08/791,765
FILING DATE: (UNKNOWN)
APPLICATION NUMBER: 09/471,765
FILING DATE: (UNKNOWN)
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
FELEROMOUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.9%; Score 47.5; D
Best Local Similarity 33.3%; Pred. No. 1.7;
Matches 8; Conservative 5; Mismatches
                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/969,834
FILING DATE: 01-0ct-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-969-834-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1326, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-925-301-1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1326
LENGTH: 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                       3,
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1326
                                                                                                                                               96 GXGLKSXECVRLLXLXXXAFPVDTNVGRLXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQ 155
                                                                                                                                                                                      225 GVGRYTAGAIASIAFGOATGVVDGNVARVLCR-------VRAIGADPSSTLVS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 758;
                                                               Length 486;
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 468, Application US/09741669
Fatent No. US2002022718A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: Genes identified as CORRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILIAG DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
                                                                                                                                                                                                                                156 KXLWPRLCKLXQ-XTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                        271 QOLWGLAQQLVDPARPGDFNQAAMELG-ATVCTPQRPLCSQCPV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
19;
                                                               10;
                                                             6.6%; Score 46; DB 10
18.3%; Pred. No. 12;
tive 12; Mismatches
                                                       DB
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 46; DB
illarity 46.2%; Pred. No. 19;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFWARE: Patentin version 3.0
SEQ ID NO 224
LENGTH: 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/801,368 CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. US20020128250Alman, Thea
Royer, John
Salama, Sofile
Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 LXXXAFPVDTNVGRIXVRXGXVPLXP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 LONSAFPPDIN--RIAPANNIMPLQP 533
                                                                                                                                                                                                                                                                                                                                                                               Sequence 224, Application US/09801368 Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-224
                                                             Query Match
Best Local Similarity 18.3%
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Busby, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cali, Brian
Hecht, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maxon, Mary
Milne, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                              US-09-801-368-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-741-669-468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                 ò
                                                                                                                                                                                        pp
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                          Pp
```

1;

Gaps

```
1;
                                                                                                                                                                                                                                                                                                             Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 146;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09969834
Patent No. US20020102711A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
PROTEIN
                                                                                                                                                                                                                                                                                                          Score 47.5; DB 10;
Pred. No. 1.4;
5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47.5; DB 10;
Pred. No. 1.7;
5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: CA99/00717
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION: Human Cystatin E FILE OF INVENTION: Human Cystatin E FILE OF INVENTION NUMBER: US/09/940,497 CURRENT FILING DATE: 2001-08-29 PRIOR APPLICATION NUMBER: US 08/744,138 PRIOR APPLICATION NUMBER: US 08/461,030 PRIOR FILING DATE: 1996-11-05 PRIOR PPLICATION NUMBER: US 08/461,030 PRIOR FILING DATE: 1995-06-05 NUMBER OF SEQ ID NOS: 13 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 YFLDVELGRTT-CTKTQPNLDNCP 110
                                                                                                                                                                                                                                                                                                                                                                                                174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-940-497-3
; Sequence 3, Application US/09940497
; Patent No. US20020052476A1
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.98;
                                                                                                                                                                                                                                                                                                             6.9%;
ilarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-775-932-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-940-497-3
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-969-834-3
                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                      APPLICANT: Ruben et al. TITLE OF INVENTION: Calcium Channel Polynucleotides, Polypeptides, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 PVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 PSPTHASRLPIR----PFLVITAYGD-HILRFFFPAQDSEDFSLYPMSCYIHIYTLFVLYV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CÜRRENT FILING DATE: 2001-01-17

Prior application data removed · refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1188

LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9%; Score 47.5; DB 10; Length 82; 22.2%; Pred. No. 0.91; ive 10; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9; Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: University of British Columbia
TITLE OF INVENTION: Production and use of Modified Cystatins
FILE REPERENCE: 58069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50.5; DB 9;
Pred. No. 2.6;
2; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 LWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 LLPRMASLG-LTLLIFYYSFAIVGMEFFCGIVFPNC 365
                                                      TITLE REPERENCE: PT01391C1
CURRENT APPLICATION NUMBER: US/10/050,786
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 09/774,028
PRIOR APPLICATION NUMBER: US 09/774,028
PRIOR APPLICATION NUMBER: US 06/774,028
PRIOR APPLICATION NUMBER: US 06/145,958
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/145,958
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1188, Application US/09764877 Patent No. US20020147140A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09775932 Patent No. US20020137671A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.3%;
Best Local Similarity 36.1%;
Matches 13; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.9%
Best Local Similarity 22.2%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-050-786-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-764-877-1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 XXI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 FSV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-775-932-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

Gaps

3;

```
; ORGANISM: Leishmania major and chagasi
US-09-874-923-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 121, Application US/09874923; Patent No. US20020081320A1; CENERAL INFORMATION: APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 7, Application US/10050786
; Patent No. US20020155539A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-874-923-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-10-050-786-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 GXGLKSXE-CVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/09874923

Sequence 22, Application US/09874923

Patent No. US20020081320A1

SGENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Webb, John R.

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Polit, Rhea

APPLICANT: Probst, Peter

APPLICANT: Probst, Peter

APPLICANT: Probst, Peter

APPLICANT: Trice of INVENTION: LISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: LISHMANIA ANTIGENS FOR LEISHMANIASIS

FILE REFERENCE: 210121.42C8

CURRENT FILING DATE: 2001.06-04

NUMBER OF SEQ ID NOS: 122

CURRENT: SactSEQ for Windows Version 4.0

SEQ ID NO 22

LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 320;
                                                                                                                                                                                                                                                                  Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 ------CPCTDPNCASCPSDAGTC 92
                                                                                                                                                                                                                                                           Score 57.5; DB 10; Length
Pred. No. 0.037;
4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55.5; DE Pred. No. 0.2; 7; Mismatches
PRIOR FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: US 08/744,138
PRIOR FILING DATE: 1996-11-05
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESUL: 4

US 09-874-923-55

Sequence 55, Application US/09874923

Sequence 55, Application US/09874923

GENERAL INFORMATION:
APPLICANT: Read, Steven G.
APPLICANT: Webb, John R.
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
                                                                                                                                                                                                                                                                                                                                                              :| : ||: ||| || : ||
84 YYFNVKFGRTT-CTKSQPNLDNCP 106
                                                                                                                                                                                                                                                                                                                                         174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.0%;
Best Local Similarity 19.3%;
Matches 21; Conservative 7
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Leishmania major
US-09-874-923-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                  ; ORGANISM: Homo sapiens US-09-940-497-4
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-874-923-22
                                                                                                                                                             LENGTH: 142
                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
96 GXGLKSXE-CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 GXGLKSXE-CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Campos-Netco, Autonio
APPLICANT: Campos-Netco, Autonio
APPLICANT: Webb, John R.
APPLICANT: Billon, Davin C.
APPLICANT: Blatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Brain, Ajay
APPLICANT: Probst, Peter
APPLICANT: Probst, Peter
APPLICANT: Probst, Peter
APPLICANT: Probst, Peter
TILLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TILLE OF INVENTION: LEISHMANIA IN DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C8
CURRENT PLLICATION NUMBER: US/09/874,923
CURRENT FILICATION NUMBER: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 709;
APPLICANT: Probst, Peter;
APPLICANT: Brannon, Mark
TITLE OF INVEWION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVEWION: LEISHMANIA AND DIAGNOSIS OF LEISHMANIASIS
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C8
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 320
TYPE: RAT
TYPE: RAT
ORGANISM: Leishmania major
US-09-874-923-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----CPCTDPNCASCPSDAGTC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 GYGLTSSSVCVRCSVAGCKSCPVDANVCKVCL-GGSEPINNM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.0%; Score 55.5; DB 10; Best Local Similarity 19.3%; Pred. No. 0.2; Matches 21; Conservative 7; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.0%; Score 55.5; DB 10;
ilarity 19.3%; Pred. No. 0.47;
Conservative 7; Mismatches 30;
```

ä

```
; ORGANISM: Homo sapiens US-09-775-932-10
                                                                                                                                                                                                                                                                                     US-09-775-932-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-940-497-4
                                                                                44
00
. . 444444444
& ~ 00000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4. Appl
Sequence 22, Appl
Sequence 121, Appl
Sequence 118, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1326, Appli
Sequence 224, Appli
Sequence 35736, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Appl
                                                  2002, 19:26:04; Search time 7.14052 Seconds (without alignments) 464.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-764-877-1188
US-09-775-932-2
US-09-940-497-3
US-09-969-834-1326
US-09-925-301-1326
US-09-741-669-468
US-09-864-761-35736
US-09-876-322-6
US-09-940-497-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-940-497-4

US-09-874-923-22

US-09-874-923-55

US-09-874-923-121

US-10-050-786-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-775-932-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-818-954A-3
US-09-943-388-2
                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-943-388-9
                                                                                                                                                      92612 seqs, 14418503 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                    - protein search, using sw model
                                                                                                                                                                                                                                       Listing first 45 summaries
                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 1008
                                                                                                                                                                                           seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-840-743-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                     November
                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                           Minimum DB
Maximum DB
                                   OM protein
                                                                                                                                                                                                                                                          Database :
                                                                                                           Sequence:
                                                                                                                                                       Searched:
                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
```

```
20 44 6.3 130 9 US-09-943-388-5 Sequence 5, Appli 22 44 6.3 130 10 US-09-818-954A-1 Sequence 176, Appli 23 44 6.3 146 10 US-09-925-299-776 Sequence 776, Appli 24 6.3 216 10 US-09-76-1367 Sequence 776, Appli 24 6.3 661 10 US-09-764-853-607 Sequence 776, Appli 25 43 6.2 213 10 US-09-764-853-667 Sequence 6507, Appli 27 43 6.2 213 10 US-09-764-853-652 Sequence 6507, Appli 28 6.2 213 10 US-09-764-853-652 Sequence 6507, Appli 29 43 6.2 213 10 US-09-764-853-652 Sequence 6507, Appli 29 43 6.2 213 10 US-09-764-853-652 Sequence 6507, Appli 31 42.5 6.1 121 10 US-09-764-853-652 Sequence 67, Appli 32 42 6.1 141 10 US-09-764-853-652 Sequence 67, Appli 33 42 6.1 162 10 US-09-764-86 Sequence 349, Appli 34 42 6.1 162 10 US-09-764-80 Sequence 349, Appli 36 42 6.1 162 10 US-09-764-80 Sequence 70, Appli 36 42 6.1 162 10 US-09-764-80 Sequence 8, Appli 37 42 6.1 162 10 US-09-764-80 Sequence 70, Appli 36 42 6.1 1203 9 US-09-90-00-65 Sequence 27, Appli 44 41.5 6.0 11 10 US-09-90-00-67 Sequence 27, Appli 44 41.5 6.0 118 10 US-09-914-8 Sequence 27, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 27, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 118 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 141 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 141 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 141 10 US-09-914-91 Sequence 7, Appli 44 41.5 6.0 140 497-5 Sequence 7, Appli 44 41.
```

## ALIGNMENTS

```
US-09-775-932-10
US-09-775-932-10
US-09-775-932-10
US-09-775-932-10
US-09-775-932-10
US-09-775-932-10
US-09-775-932-10
US-08-ENEWENTON: Production and use of Modified Cystatins
FILE REPERBUCE: 58069-10-2-02
US-08-ENING DATE: 1099-08-05
PRIOR APPLICATION NUMBER: 05/09/0717
PRIOR APPLICATION NUMBER: 05/09/0717
PRIOR APPLICATION NUMBER: 06/095/503
PRIOR APPLICATION NUMBER: 06/095/503
PRIOR PILING DATE: 1998-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR PRIOR APPLICATION NUMBER: 05/09/940,497
PRIOR PRIOR DATE: 1999-08-05
PRIOR PRIOR DATE: 2.001-08-29
PRIOR PRIOR DATE: 2.001-08-29
PRIOR PRIOR DATE: 2.001-08-29
PRIOR PRIOR DATE: 2.001-08-29
PRIOR PAPLICATION NUMBER: 05/09/241,376
```

;

THIS PAGE BLANK (USPTO)

```
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                 103 ECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
7.0%; Score 48.5; DB 1; Length 259;
Best Local Similarity 23.4%; Pred. No. 2.9;
Matches 22; Conservative 7; Mismatches 38; Indels 27; Gaps

      SMART; SM00478; ENDO3c; 1.

      SMART; SM00525; FES; 1.

      PROSITE; PS00164; ENDONUCLEASE_III_1; 1.

      PROSITE; PS01155; ENDONUCLEASE_III_2; 1.

      Hypothetical protein; DNA repair; Hydrolase; Glycosidase; Lyase; Iron-sulfur; 4Fe-4S.

      METAL
      187

      METAL
      194

      197
      IRON-SULFUR (4FE-4S) (BY SIMILARITY).

      METAL
      197

      METAL
      203

      187
      1RON-SULFUR (4FE-4S) (BY SIMILARITY).

      METAL
      203

      180
      1RON-SULFUR (4FE-4S) (BY SIMILARITY).

      SEQUENCE
      259 AA; 28841 MW; F52E57810571EDBC CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 CKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

Search completed: November 8, 2002, 19:27:11 Job time : 10.268 secs

```
"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ainscough R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  END3_CAEEL
P54137;
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    END3_CAEEL
                                                                                                                                                                                                                                                                                                                               ò
QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A WOOd V. Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., RA Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Ra Brooks K., Brown D., Brown S., Chiling Writer C.M., A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gonlins M., Connor R., Davis P., Feltwell T., Fraser A., Gonlins M., Connor R., Marris D., Hidalgo J., Hodgson G., R. James K., Jones L., Jones M., Laather S., McDonald S., McLean J., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., R. James R., Jones M., Squares S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., A Woodward J., Volckaert G., Askelton J., Whitehead S., Mocdward J., Volckaert G., Askelton J., Grymonprez B., Meltjens I., Vanstreels E., Rieger M., Scheefer M., Mueller-Auer S., Rabelt C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabelt C., Fuchs W., Medler H., Wanbutt R., Pohl T.M., Ber P., Zimmermann W., Wedler H., Wanbutt R., Purnelle B., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Angar R., Calibert I., Moreno S., Armstrong J., Forsburg S.L., Ra Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Ra Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           Gaps
          "Nucleotide sequence of the essential region of bacteriophage P4.";
Nucleic Acids Res. 12:8667-8684(1984).
-:- SIMILARITY: SOME, TO E.COLI PROPHAGE CP4-57 REGULATORY PROTEIN
                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                             DB 1; Length 88;
                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                       132 PLXPLPXXXQXHXLXXYPXXXXXQKXLWP---RLCKLXQXTLYEL 173
                                                                                                                                                                                                    EMBL; X51522; CAA35903.1; -.
EMBL; X02534; CAA26377.1; -.
PIR; G23878; Q1BPP4.
PIR; JW0029; JW0029.
PIR; JW0029; JW0029.
DNA_BIND 30 49 H-T-H MOTIF (POTENTIAL).
SEQUENCE 88 AA: 9749 MW; DA16EF6EBB7BD70F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          15 PLMPLPDITQERFLRV------PEVMHLCGLSRSTIYEL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
19-JUL-1001 protein C2068.09c in chromosome 1
SPAC2068.09C.
                                                                                                                                                                                                                                                                                                                          Score 49.5; DB Pred. No. 0.69; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                         7.1%;
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDK9_SCHPO
P87115;
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDK9_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HAS BOTH AN APURINIC AND/OR APYRIMIDINIC ENDONUCLEASE
ACTIVITY AND A DNA N-GLYCOSYLASE ACTIVITY (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate.
-!- COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE BUNYME ALONG THE DNA STRAND (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
Probable endonuclease III homolog (EC 4.2.99.18) (DNA-(Apurinic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 49; DB 1; Length 1033; 27.9%; Pred. No. 9.1; Live 6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 289 ATP (POTENTIAL).
1033 AA; 116463 MW; 8432B313DB18E135 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 KXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; ATP-binding; Nuclear protein. NP_BIND 282 289 ATP (POTENTIAL).
Nature 415:871-880(2002).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: BELONGS TO THE UPF0202 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wormbep; R10E4.5; CE03559.
InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004035; EndoIII_HhH.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; FeS_bind.
Pfam; PF00730; HhH-GPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z50874; CAA90766.1; -. HSSP; P20625; 2ABK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 295334; CAB08603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apyrimidinic site) lyase). R10E4.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 27.9
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
```

σ

Matches 92

ŏ g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilensib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halling C., Calendar R., Christie G.E., Dale E.C., Debo G., Finkel S., Flensburg J., Ghisotti D., Kahn M.L., Lane K.B., Lin C.-S., Lindqvist B.H., Pierson L.S., Six E.W., Sunshine M.G., Ziermann R.; "DNA sequence of satellite bacteriophage P4."; Nucleic Acids Res. 18:1649-1649(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-077-1989 (Rel. 12, Created)
01-077-1989 (Rel. 12, Last sequence update)
01-077-1994 (Rel. 30, Last annotation update)
Hypothetical 9.7 kDa protein (ORF88) (Putative DNA-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                 01-0cT-1996 (Rel. 34, Last sequence update)
15-JUV-2002 (Rel. 41, Last annotation update)
Hypothetical 119.3 kDa protein in FPR1-TOM22 intergenic region.
YML132W OR N1216 OR N1858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
unclassified Myoviridae.
NCBL_TaxID=10680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.4%; Score 51; DB 1; Length 1056; 30.2%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).

M; 76721ED0867ED618 CRC64;
                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 KXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703 KTLPPLLIKLSEQPPHYLHYLGVSYGLTQSLHKFWKNNSFVPV 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 246843; CAA86893.1; -.
BMBL; 271408; CAA96014.1; -.
SGD; SO005076; YRL132w.
Hypothetical protein; ATP-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90221913; PubMed=2183201;
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96109932; PubMed=8619318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-85062840; PubMed-6095206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 1056 AA; 119347 MW;
                                                                                                              34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 13; Conserv
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage P4.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                              01-OCT-1996
                                                                 YNN2_YEAST
P53914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y9K_BPP4
P12552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
                                            YNN2_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y9K_BPP4
                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98037514; PubMed-9371463;
A Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook K., Gibbert K., Aldredge T., Bashirzadeh P., Lumm W., Pothier B., Qiu D., Adardora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jawan I., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Peterbowski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).

C. PUNCTION: DNA REPRIXE REXYME THAT INCISES DNA AT 8-OXG RESIDUES. EXCISES 7.8-DIMYDRO-8-OXGGINANINE AND 2.6-DIAMINO-4-HYDROXY-5-N-METHYLFORMAMIDOPMINIDINE (RAPY) FROM DAMAGED DNA. HAS A BETALYLFORMAMIDOPMINIDINE (RAPY) FROM DAMAGED UNA. HAS A BETALYLFORMAMIDOPMINITY: Endonucleolytic cleavage near apurinic or apyrimidaline sites to products with 5'-phosphate.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
19robable N-glycosylase/DNA.lyase [Includes: 8-oxoguanine DNA glycosylase (EC 3.2.2.); DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP lyase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRPAMS; TIGR00588; ogg; 1.
Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                            LEWLRXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXX-XAFPVDTNVGRIXVR 127
                                                                    Methanobacterium thermoautotrophicum.
Archaea; Euryarchheota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 312;
30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D33B4FF497BC5A1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.4%; Score 51.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 LLXXXGXGLKSXECVRLLXL-XXXAFPVDTNVGRI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 LLELSGVGPKVADCILLYGFRKTEAFPVDVWIRRI 260
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multifunctional enzyme; Complete proteome. ACT_SITE 235 235 BY SIMILARITY
                                                                                                                                                                                                     312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000897; AAB85820.1; -. InterPro; IPR003265; Endo_3c. InterPro; IPR003583; HHH_I. InterPro; IPR004577; Ogg. Pfam; PR00730; HHH-GPD; I. SMART; SM00478; ENDO3c; I. SMART; SM00278; HHH1; I.
9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 40.0
Matches 14; Conservative
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
16;
                                                                                                                                                                                                  OGG1_METTH
O27397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                       MTH1342
```

ò 셤

ö

ó

Indels

```
SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE-98012228; PubMed-9348312;
Kuo F.C., Sklar J.L.;
*Augmented expression of a human gene for 8-oxoguanine DNA glycosylase (MutM) in B lymphocytes of the dark zone in lymph node germinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bolteux S., Radicella J.P.; "The human OGG1 gene: structure, functions, and its implication in the process of carcinogenesis.";
               yeast OGG1 gene that is involved in ";
                                                                                                                                                                                                                              "Opposite base-dependent reactions of a human base excision repair enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites."; EMBO J. 16:6314-6322(1997).
Morishita K., Shinmura K., Kohno T., Taniwaki M., Ohwada S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-99250167; PubMed-10233168;
Mishioka K., Ohtsubo T., Oda H., Fujiwara T., Kang D., Sugimachi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Expression and differential intracellular localization of two major forms of human 8-Oxoguanine DNA glycosylase encoded by alternatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99428653; PubMed-10497264; Dherin C., Radicella J.P., Dizdaroglu M., Boiteux S.; Excision of oxidatively damaged DNA bases by the human alpha-hoggl protein and the polymorphic alpha-hoggl(Ser336Cys) protein which is frequently found in human populations.",
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1A).
Dhenaut A., Boiteux S., Radicella J.;
"Genomic structure and promoter characterization of the human 8-OH-guanine glycosylase gene (OGG1) gene.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chevillard S., Radicella J.P., Levalois C., Lebeau J., Poupon M.F., Oudard S., Dutrillaux B., Boiteux S.; "Mutations in OGG1, a gene involved in the repair of oxidative DNA damage, are found in human lung and kidney tumours.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shinmura K., Kohno T., Kasai H., Koda K., Sugimura H., Yokota J., "Infrequent mutations of the hOGG1 gene, that is involved in the excision of 8-hydroxyguanine in damaged DNA, in human gastric
                                                                                                                                                                                                         Bjoras M., Luna L., Johnsen B.E., Hoff E., Haug T., Rognes T.,
                                                                                                                                                                                                                                                                                                                                                                SEQÜENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-99380087; PubMed-10449904;
Biblida T., Hippo Y., Nakahori Y., Matsushita I., Kodama T.,
Nishimura S., Aburatani H.;
"Structure and chromosome location of human OGG1.";
Cytogenet. Cell Genet. 85:232-236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arch. Biochem. Biophys. 377:1-8(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jpn. J. Cancer Res. 89:825-828(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION OF VARIANT CYS-326.
                        "Cloning of a human homolog of the
the repair of oxidative DNA damage.
Oncogene 14:2857-2861(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. Cell 10:1637-1652(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20239648; Pubmed-10775435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98438755; PubMed-9765618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98324718; PubMed-9662341;
                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE-98026907; Pubmed-9321410;
                                                                                                                                                       J. Exp. Med. 186:1547-1556(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 16:3083-3086(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spliced OGG1 mRNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT HIS-154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT GLN-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakabeppu Y.;
                                                                                                                                                                                                                      Seeberg E.;
             Yokota J.;
                                                                                                                                            centers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multifunctional enzyme; Nuclear protein; Mitochondrion;
Alternative splicing; Polymorphism.
ACT_SITE 249 249 BY SIMILARITY.
VARSPLIC 317 345 VLESADLRQSRHAQEPPAKRRKGSKGPEG -> VSVPRCPP
(IN ISOPORM 18).
VARSPLIC 317 345 VLESADLRQSRHAQEPPAKRRKGSKGPEG -> TPPSYRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPFPTSLSPSPPSLMLGRGLPVTTSKARHPQIKQSVCTTRWGGGY (IN ISOFORM 1C).
VLFSADLRQSRHAQEPPAKRRKGSKGPEG -> GLLGNAFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHQLLRPLIFCQDHLREGPP1GRGDSQGEELEPQLPSSLSS
IPYGFCDHCWTKDVDDPPLVTHPSPGSRDGHMTQAWPVKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPLATVIGHVMQASLLAL (IN ISOFORM 2A).
VADCICLMALDKPQAVPVDVHMWHIAQRDYSWHPTTSQAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVPTCANPAMLRSHQQSAERVPKGRKARWGTLDKEIPQAPS
                                                                                                                                                                     found in human tumors on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISOFORM 2A).

ALTERNATUS PRODUCTS: 8 ISOFORMS; 1A/ALPHA (SHOWN HERE), 1B, 1C, 2A/BETA, 2B, 2C, 2D AND 2E; ARE PRODUCED BY ALTERNATIVE SPLICING. 1A IS THE PREVALENT FORM.
                                                             MEDLINE-20368626; PubMed=1908322;
Audebert M., Radicella J.P., Dizdaroglu M.;
Audebert M., Radicella J.P., Dizdaroglu M.;
Audebert M., Radicella J.P., Dizdaroglu M.;
Effect of single mutations in the OGG1 gene found in human tumors of the substrate specificity of the Ogg1 protein.";
Nucleic Acids Res. 28:3672-3678(2000).
I. FUNCTION: DNA REPAINE ENZYME THAT INCISES DNA AT 8-OXOG RESIDUES.
EXCISES 7,8-DIMYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-METHYLFORMAMIDOPYRIMIDINE (FAPY) FROM DAMAGED DNA. HAS A BETA-I-CARALYTIC ACTIVITY: Endonucleolytic cleavage near apurinic or apyrimidianic sites to products with 5'-phosphate.
I. SUBCELLIGAR LOCATION: NUCLEAR (ISOFORM IA) AND MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO0588; ogg; 1.
Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: UBIQUITOUS.
DISEASE: DEFECTS IN OGG1 ARE ASSOCIATED WITH TUMOR FORMATION.
SIMILARITY: BELONGS TO THE OGG1 FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53.5; DB 1;
Pred. No. 0.57;
Nucleic Acids Res. 27:4001-4007(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL. Y11818 CAA72536.1)
EMBL. Y11711, CAA72414.1;
EMBL. AB000410; BAA19103.1;
EMBL. AB000410; BAA19103.1;
EMBL. GBS27; AAB68614.1;
EMBL. Y13277; CAA73726.1;
EMBL. Y13277; CAA73726.1;
EMBL. AT31341; CAA1055.1;
EMBL. AF086891; AAB41680.1;
EMBL. AF088822; AAD41681.1;
EMBL. AB019528; BAA76635.1;
EMBL. AB019528; BAA76635.1;
EMBL. AB019539; BAA76635.1;
EMBL. AB019539; BAA76636.1;
EMBL. AB019539; BAA76638.1;
EMBL. AB019531; BAA76638.1;
EMBL. AB019531; BAA76638.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003265; Endo_3c.
InterPro; IPR004577; Ogg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U96710; AAB81132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.78;
30.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC:8125; OGG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00730; HhH-GPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew;
```

4

```
Query Match
Best Local (
                                                  96
                                                                            116
                         Matches
                                                                                                                                                                     RESULT 10
                                                                                                                              Оp
                                                                                                                                                                                               g
                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRANH-LTZ / SGSC1412 / ATCC 700720;
MEDLINE-2134948; PubMed=11677609;
MCDLINE-2134948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nayyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         NACULE 413:52-836 (2001).

-1- FUNCTION: ADERINE GITCOSYLASE ACTIVE ON G-A AND C-A MISPAIRS.
-1- COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYIT CATIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE BIXEM ALONG THE DNA STRAND (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON-SULFUR (4FE-45) (BY SIMILARITY).
IRON-SULFUR (4FE-45) (BY SIMILARITY).
IRON-SULFUR (4FE-45) (BY SIMILARITY).
SCS5DB4D7B7BB69F CRC64;
                                                                                                                                                                                                                                  Desiraju V., Shanabruch W.G., Lu A.L.; "Nucleotide sequence of the Salmonella typhimurium mutB gene, the homolog of Escherichia coli mutY."; Decteriol. 175:541-543(1993).
                                                                                                                              Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
DNA repair; Hydrolase; Glycosidase; Iron-sulfur; 4Fe-4S;
                                                         Ol-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ACG-Specific adenine glycosylase (EC 3.2.2.-)
MUTX OR MUTB OR STM3110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE008843; AAL21985.1; -. PIR; A40647; A40647. HSSP; P17802; JMU. StyGene; SG10238; mutx. InterPro; IPR004035; EndoIII_FCL. InterPro; IPR004035; EndoIII_HH. InterPro; IPR004035; EndoIII_HH. InterPro; IPR003265; EndoIII_HH. InterPro; IPR003631; FeS_bind. InterPro; IPR003583; HHH_1.
                                                                                                                                                                                                                      MEDLINE-93123173; PubMed-8419300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39409 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M86634; AAA27165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIGRFAMS; TIGR01084; mutY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00730; HhH-GPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:852-856(2001)
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192
199
202
208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00278; HhH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
202
208
350 AA;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                    NCBI_TaxID=602;
                                                                                                                                                                                                           STRAIN-GW1803;
                                 MUTY_SALTY
Q05869;
                                                                                                                                                         Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
SEQUENCE
                        MUTY_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
            RESULT 9
```

```
SEQUENCE FROM N.A. (ISOFORM 2).
MEDILINE-9738611; Pubmed-9223306;
ROldan-Arijona T., Wei Y.-F., Carter K.C., Klungland A., Anselmino C.,
Wang R.-P., Augustus M., Lindahl T.;
"Molecular cloning and functional expression of a human cDNA encoding
the antimutator enzyme Bhydroxyguanine-DNA glycosylase.";
proc. Natl. Acad. Sci. U.S.A. 94:8016-8020(1997).
                                                                                                                                                        GXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQ 155
                                                                                                                                                                                                                             GVGRSTAGAILSLALGKHYPILDGNVKRVLAR------------CYAVSGWPGKKEVE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABDLINE-97330655; PubMed-9187114;
Aburatani H., Hippo Y., Ishida T., Takashima R., Matsuba C.,
Kodama T., Takao M., Yasui A., Yamanoto K., Asano M., Fukasawa K.,
Yoshinari T., Inoue H., Otsuka E., Nishimura S.;
"Cloning and characterization of mammalian 8-hydroxyguanine-specific
DNA 91ycosylase/apurinic, apyrimidinic lyase, a functional muth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Radicella J.P., Dherin C., Desmaze C., Fox M.S., Boiteux S.; "Cloning and characterization of hOGG1, a human homolog of the OGG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OGGI_HUMAN STANDARD; PRT; 345 AA.
OGGI_HUMAN STANDARD; PRT; 345 AA.
O15527; O00390; P78554; O00670; O00705; O14876; O95488; Q9UL34;
O97653; O97664; Q9UIKO; Q9UIKI; Q9UIKZ; Q9Y2C1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
N-G1ycosylase/DNA lyase [Includes: 8-oxoguanine DNA glycosylase (EC 3.2...); DNA-(apurinic or apyrimidinic site) lyase
CEC 4.2.99.18) (AP lyase)].
OGGI OR MMH OR MUTM OR OGHI.
                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A mammalian DNA repair enzyme that excises oxidatively damaged guanines maps to a locus frequently lost in lung cancer."; Curr. Biol. 7:397-407(1997).
                                                                                                                                                                                                                                                                                                         156 KXLWPRLCKLXQXTLYE------LHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                              162 NTLW-----TLSEQVTPARGVERFNQAMMDLG-AMVCTRSKPKCTLCPL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE=97352815; Pubmed-9207108;
ROSenquist T.A., Zharkov D.O., Grollman A.P.;
"Cloning and characterization of a mammalian 8-oxoguanine DNA
   Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 94:7429-7434(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene of Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 94:8010-8015(1997).
       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                             0.33;
                                                                                12; Mismatches
       Score 55;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [5] SEQUENCE FROM N.A. (ISOFORM 1A). MEDLINE-97342862; PubMed-9197244; Lu R., Nash H.M., Verdine G.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE=97368310; Pubmed=9223305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE=97334205; PubMed=9190902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer Res. 57:2151-2156(1997).
7.98;
                                                                                22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosylase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homologue.
```

```
Bjoras M., Luna L., Johnsen B.E., Hoff E., Haug T., Rognes T.,
TISSUE-Lung;
MEDLINE-98026907; PubMed-9321410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
    NAMES OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic structure and chromosomal localization of the mouse Oggl gene that is involved in the repair of 8-hydroxyguanine in DNA damage."; Mamm. Genome 9:32-37(1998).
                                                                                                                                                                                         AP LYASE ACTIVITY.
K->R: DIMINISHES BOTH DNA GLYCOSYLASE AND
AP LYASE ACTIVITY.
                                                                                                                                                                         K->Q: ABOLISHES BOTH DNA GLYCOSYLASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=97330655; Pubmed=9187114;
Aburatani H., Hippo Y., Ishida T., Takashima R., Matsuba C.,
Kodama T., Takao M., Yasui A., Yamamoto K., Asano M., Fukasawa K.,
Yoshinari T., Inoue H., Otsuka E., Nishimura S.,
"Cloning and characterization of mammalian 8-hydroxyguanine-specific
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                         Lyase; DNA repair; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OGGI_MOUSE STANDARD; PRT; 345 AA.
008766; 008991; 035915; 035617; 008733; 008910; 090XE8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-OCT-2011 (Rel. 40, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97342862; PubMed-9197244;
Lu R., Nash H.M., Verdine G.L.;
A mammalian DNA repair enzyme that excises oxidatively damaged guanines maps to a locus frequently lost in lung cancer.";
Curr. Biol. 7:397-407(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA glycosylase/apurinic, apyrimidinic lyase, a functional mutM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97352815; PubMed-9207108; Rosenquist T.A., Zharkov D.O., Grollman A.P.; "Cloning and characterization of a mammalian 8-oxoguanine DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tani M., Shinmura K., Kohno T., Takenoshita S., Nagamachi Y., Yokota J.;
                                                                                                                                                                                                                                                                                                  DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                          4ADB72EB20E4BF20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proc. Natl. Acad. Sci. U.S.A. 94:7429-7434(1997)
                                                                                                                                                                                                                                                                                                                                                                                   91 LLXXXGXGLKSXECVRLLXLXXXAF-PVDTNVGRIXVR 127
                                                                                                                                                                                                                                                                                                                                                                                                             Score 56.5; DB Pred. No. 0.2; 4; Mismatches
                 InterPro; IPR004577; Ogg.
Pfam; PF00730; HhH-GPD; 1.
SMRAT; SM00478; ENDO3C; 1.
TIGRPAMS; TIGR00588; Ogg; 1.
Hydrolase; Nuclease; Endonuclease; Lyase; Multifunctional enzyme; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98096582; PubMed=9434942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer Res. 57:2151-2156(1997)
                                                                                                                                                                                                                                                          376 AA; 42781 MW;
  IPR003265; Endo_3c.
                                                                                                                                                                                                                                                                                                8.2%;
llarity 39.5%;
Conservative
                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                         241
                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nomologue.
  InterPro;
                                                                                                                                                 ACT_SITE
MUTAGEN
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                               MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OGG1_MOUSE
                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
  ô
                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
"Opposite base-dependent reactions of a human base excision repair enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites."; EMBO J. 16:6314-6322(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                             glycosylase ligene (OGH).";
Submitted (AuG-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA REPAIR EMZYME THAT INCISES DNA AT 8-0XOG RESIDUES.
EXCISES 7,8-DIMYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-
NETHYLEORMAMIDOPYRIMIDINE (FARY) FROM DAMAGED DNA. HAS A BETA-
LYASE ACTIVITY THAT NICKS DNA 3' TO THE LESION.
-!- CAMPLYTC ACTIVITY: Endonucleolytic cleavage near apurinic or
apyrimidinic sites to products with 5' phosphate.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TESTIS.
-!- SIMILARITY: BELONGS TO THE OGGI FAMILY 1.
                                                                                                                                                                                                                                                                                                                                   Johnsen B., Luna L., Rognes T., Seeberg E.; "Complete genomic DNA sequence of the Mus musculus 8-oxoguanine DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003265; Endo_3c.
InterPro; IPR004577; Ogg.
InterPro; IPR004577; Ogg.
InterPro; IPR004781; HhH-GPD; 1.
SMART; SM00478; EnDO3c; 1.
TIGRRAMs; TIGR0588; Ogg; 1.
Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEWLRXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXX-XAFPVDTNVGRIXVR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55.5; DB 1; Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . terpro; ...
. terpro; ...
. terpro; ...
. nterpro; ...
. nterpro; ...
. nterpro; ...
. pfam; PF0030; hHr-Gr.,
. SMART; SM0478; ENDO3c; 1.
. TIGREAMS; TIGRO588; ogg; 1.
. TIGREAMS; TIGRO588; ogg; 1.
. Hydrolase; Nuclease; Endonuclease; Lyac.
. Multifunctional enzyme; Nuclear protein.
. ACT_STE 249 249 BY SIMILARITY.
. ACT_STE 249 249 BY SIMILARITY.
. ACT_STE 240 S -> Q (IN REF. 2).
. TCT 23 25 WAS -> SQ (IN REF. 2).
. 239 A -> G (IN REF. 1).
. C -> S (IN REF. 1).
. S -> F (IN REF. 1).
. H (IN REF. 5 AND 7 CRC).
                                                                                                                                                      STRAIN=C57BL/6J;
Radicella J.P., Reille F., Dherin C., Boiteux S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75BB0DDB084E4947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF003596; AAB61289.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ001307; CAB65240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y11247; CAA72117.
EMBL; Y13479; CAA73883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1097693; Ogg1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U96711; AAB81133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
```

ıO

ï

Gaps

Indels

29;

Mismatches

; 9

Conservative

```
17;
                                                                                                                                                                                                                                                      OGG1_YEAST
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----
                                                                                                                                                                                                                            RESULT
                                                                οy
                                                                                                                           q
                                                                                                                                                                                                                                                                                       4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                              LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                  .- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prieto Alamo M.J., Jurado J., Francastel E., Laval F.;
"Rat 7,8-dihydro-8-oxoguanine DNA glycosylase: substrate specificity,
kinetics and cleavagemechanism at an apurinic site.";
Nucleic Acids Res. 26:5199-5202(1998).
-!- FUNCTION: DNA REPAIR ENZYME THAT INCISES DNA AT 8-OXOG RESIDUES.
EXCISES 7.8-DIHYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-
METHYLEORMAMIOPYRIMIDINE (FAPY) FROM DAMAGED DNA. HAS A BETA-
LYASE ACTIVITY THAT NICKS DNA 3' TO THE LESION.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage near apurinic or
apyrimidinic sites to products with 5'-phosphate.
-!- SUBCELLULAR LOCATION:
Nuclear (By similarity).
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Iron-sulfur; 4Fe-45; Complete proteome.
1800.FILENN-SULFUR (4FE-4S) (BY SIMILARITY).
187 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
190 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
196 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
24928 MW; D9716CD6FEFA85D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMARY, SM00478; ENDO3C; I.
TIGREAMS; TIGR00588; ogg; 1.
Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNY-2002 (Rel. 41, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
N-glycosylase/DNA lyase [Includes: 8-Oxoguanine DNA glycosylase (RC 3-22.-); DNA-(apurint or apyrimidinic site) lyase
(EC 4.2.99.91) (AP lyase)].
                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 XXXXQKXLWPR-----LCKLXQXTLY-ELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.2%; Score 56.5; DB 1; Length 213; 25.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56.5; DB 1; Length 345; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liffunctional engyme; Nuclear protein.
LISITE 249 249 BY SIMILARITY.
OUENCE 345 AA; 38711 MW; B7FDF8C782644C41 CRC64;
                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                     104 LLKLPGVGRKTANIVLWVGFKKPALAVDTHVHRISNRLGWV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 AA
                                                                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Hepatoma;
MEDLINE=99030527; PubMed=9801319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF029690; AAC77525.1; -.
InterPro; IPR003265; Endo_3c.
InterPro; IPR004577; 099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00730; HhH-GPD; 1
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                       187
190
196
                                                       187
190
196
196
213 AA;
   Lyase;
                                                                                                                                                                                                                                         Local Similarity
es 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
SEQUENCE
                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OGG1_RAT
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HERE AND DESCRIPTION OF THE PROPERTY OF THE PR
WFFFFS
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20143487; PubMed=10677220;
MEDLINE-20143487; PubMed=10677220;
Guibbourt N., Castaing B., Van Der Kemp P.A., Boiteux S.;
Guibbourt N., Castaing B., Van Der Kemp P.A., Boiteux S.;
Gutalytic and DNA binding properties of the oggl protein of Saccharomyces cerevisiae: comparison between the wild type and the K241R and K341Q active-site mutant proteins.";
Biochemistry 39:1716-1724(2000)
I: FUNCTION: DNA REPAIR ENZYME THAT INCISES DNA AT 8-OXOG RESIDUES.
EXCISES 7,8-DIHYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-METHYLFORMAMIDOPYRIMIDINE (FAPY) FROM DAMAGED DNA. HAS A BETALYABE ACTIVITY THAT NICKS DNA 3' TO THE LESION.
I'VASE ACTIVITY: Endonucleolytic cleavage near apurinic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97388538; PubMed-9241232;
Girard P. M., Guibourt N., Bolteux S.;
"The Oggl protein of Saccharomyces cerevisiae: a 7,8-dihydro-8-
oxoguanine DNA glycosylase/AP lyase whose lysine 241 is a critical
residue for catalytic activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Endonucleolytic cleavage near apurinic or apyrinidinic sites to products with 5'-phosphate.
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE OGG1 FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             van der Kemp P.A., Thomas D., Barbey R., de Oliveira R., Boiteux
"Cloning and expression in Escherichia coli of the OGGI gene of
Saccharomyces cerevisiae, which codes for a DNA glycosylase that
excises 7,8-dihydro-8-oxoguanine and 2,6-diamino-4-hydroxy-5-N-
                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
N-glycosylase/DNA lyase [Includes: 8-oxoguanine DNA glycosylase (EC 3-2.2.); DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP 19see)].
0GG1 OR YML060W OR YM9958.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetes;
                                             76 LEWLRXXXXXXXXXXXXLXXXXGXGLKSXECVRLLXXXX-XAFPVDTNVGRIXVR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C / AB972;
Devlin K., Churcher C., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccha
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 93:5197-5202(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION, AND MUTAGENESIS OF LYS-241.
                                                                                                                                                                                                                                                                376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 25:3204-3211(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96224259; PubMed=8643552;
                                                                                                                                                                                                                                                                                                                                         (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U44855; AAC49312.1; -. EMBL; Z46729; CAA86715.1; -. SGD; S0004525; OGG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methylformamidopyrimidine.
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                             01-OCT-1996
01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-FL100
                                                                                                                                                                                                                                                        OGG1_YEAST
P53397;
                                                                                                                                                                                                                                                                    HDD BERNES BERNE
```

us-09-840-743-72.rsp

DB 1; Length 142;

```
Query Match
                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>-</u>
                                                                                                                                                      RESULT
                                                                                                     g
                        RA MEDIUME-12184/49; FUDNEGE-11/80U32;

RA MEDIUME-2184/49; FUDNEGE-11/80U32;

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Balley J., Baltow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark S.Y., Clee C.M.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
R. Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Lington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gvilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.E., Johnson C.M., Johnson D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Minne S.A., Mastry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sliston J.E.,
RA Swamor R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,
R. Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swamor R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,
RA Wilting L. Wirsy P.W., Hubbard T., Durbin R.W., Bentley D.R., Williams S.A.,
RA Miling L., Wray P.W., Hubbard T., Durbin R.W., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C -> R (IN 45% OF THE POPULATION).
/FTId=VAR_002208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYSTATIN D.
REACTIVE SITE (BY SIMILARITY).
SECONDARY AREA OF CONTACT.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEFA89BA87A0DA68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00043; ČY; 1.
PROSITE; PS00287; CYSTATIN; 1.
Thiol protease inhibitor; Signal; Polymorphism.
 SEQUENCE FROM N.A.
MEDLINE-21638749; PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X59964; CAA42590.1; -.
EMBL; X70377; CAA49838.1; -.
EEMBL; AL591074; CAC94785.1; -.
PIR; S18212; S18212.
HSSP; P01034; 1G96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000010; Cystatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16080 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00031; cystatin; 1.
SMART; SM00043; CY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:2477; CST5.
MIM; 123858; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
139
46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT ARG-46.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rogers J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
Hydrolase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM THE DAWGED SITE (BY SIMILARITY).

CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apprinding site in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate.

COPACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE ENZYBE ALONG THE DNA STRAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Hochonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Fryidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.",
Nature 399:323-339(1999).

Nature 399:323-339(1999).

PUNCION: HAS BOTH AN APURINIC AND/OR APTRIMIDINIC ENDONUCLEASE
ACTIVITY AND A DNA N-GLYCOSYLASE ACTIVITY. INCISES DAMAGED DNA AT
CYTOSINES, THYMINES AND GUANINES. ACTS ON A DAMAGED STRAND, 5'
                                         Gaps
                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Endonuclease III (EC 4.2.99.18) (DNA-(apurinic or apyrimidinic site)
                                                                                                                                                                                                                                                                                                                                                                                  Thermotoga maritima.
Bacteria; Thermotogae; Thermotogae (class); Thermotogales; Thermotogaceae; Thermotoga.
                                         Indels
Score 57.5; DB Pred. No. 0.052;
                                                                                                                                                                                                                            213 AA.
                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
                                                                                174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                          :| : ||: || : ||
84 YYFNVKFGRTT-CTKSQPNLDNCP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004036; EndoIII_HHH.
InterPro; IPR003265; Endo_3c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001716; AAD35453.1; -. HSSP; P20625; 2ABK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; Fes_bind.
InterPro; IPR003583; HHH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEGURE TECNOS TO THE CAPP. 1. SMART; SMO0478; ENDO3c; 1. SMART; SMO0525; FES; 1. SMART; SMO0578; Hhill; 1. TIGREAMS; TIGRO1083; nth; 1.
                                         10; Conservative
                                                                                                                                                                                                                            STANDARD;
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                       NTH OR TM0366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; TM0366;
                                                                                                                                                                                                                          END3_THEMA
O9WYK0;
                                                                                                                                                                                                                                                                                                                                                        lyase)
                                                                                                                                                                                                         END3_THEMA
```

δ

```
Biol. Chem. 268:15737-15744(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                            EcoGene; EG10627; mutY.
InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004036; EndoIII_HHH.
                                                                                                                                                              InterPro; IPR003265; Endo_3c.
InterPro; IPR003561; Fee_bind.
InterPro; IPR003861; Fee_bind.
Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDS3c; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  350 AA; 39149 MW;
               . AE000378, AAC75998.1,
JQ0546, JQ0546.
B38535, B38535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                               1MUD; 29-OCT-99.
1MUN; 26-AUG-99.
1MUY; 20-AUG-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cystatin D precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 21; Conserv
                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTD_HUMAN
P28325;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3]
 αq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                Michaels M.L., Pham L., Nghiem Y., Cruz C., Miller J.H., "MutY, an adenine glycosylase active on G-A mispairs, has homology to endonuclease III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LAKGNT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE ENZYME ALONG THE DNA STRAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shoo Y.;
                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                               151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                   156 AAIVEKEL---LQIIDEKWLTYAHHWLILHGR-YICKARKPGCNICPI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsai-Wu J.-J., Radicella J.P., Lu A.-L.;
"Nucleotide sequence of the Escherichia coli micA gene re
A/G-specific mismatch repair: identity of micA and mutY.'
J. Bacteriol. 173:1902-1910(1991).
111 LVKLPGVGRKTANVVLNCLFAMPTMAVDTHVFRVSKRIG---
                                                                                                                                                                            01-MUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
AUG-specific adenine glycosylase (EC 3.2.2.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY
                                                                                                                                                350 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 18:3841-3845(1990)
                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90326504; PubMed=2197596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91161503; PubMed=2001994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X52391; CAA36624.1; -. EMBL; M59471; AAA72957.1; -.
                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OXOGUANINE.
                                                                                                              RESULT 3
MUTY_ECOLI
ID MUTY_ECOLI
AC P17802;
                                                                                                                                                                                                                                                                                                 Escherichia
```

```
TIGRFAMS; TIGR01084; muty; 1.
PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
DNA repair; Hydrolase; Glycosidase; Iron-sulfur; 4Fe-4S; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93340179; PubMed=8340398; Ereije J.P., Balbin M., Abrahamson M., Velasco G., Dalboge H., Grubb A., Lopez-Otin C.; "Human cystatin D. C.; "Human cystatin D. Coli expressed inhibitor, and identification of the native protein in saliva.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 GXGLKSXECVRLLXLXXXAFPV-DTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structure and expression of the gene encoding cystatin D, a novel numan cysteine proteinase inhibitor.";
J. Biol. Chem. 266:20538-20543(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-92041895; PubMed-1939105;
Freije J.P., Abrahamson M., Olafssonn I., Velasco G., Grubb A.,
Lopez-Otin C.;
                                                                                                                                                                                                                                                                                                                                              8.5%; Score 59; DB 1; Length 350; 20.2%; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                 C7D3657C03EBBF4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 ENKLWSLSEQVTPAVGVERFNQAMMDLGAMICTRSKPKCSLCPL 204
                                                                                                                                                       IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 AA
                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 0.07
14; Mismatches
```

3;

```
Rickettsia prowazekii.
                                           NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                      mitochondria.
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                          Nature 390:249-256(1997).

-:-CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal 1'-terminal 5'-phosphate.

-:-COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE ENTYME ALONG THE DNA STRAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA repair;
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosako V., Ucliyama S., Vandenbol M., Vannier F., Vassarotti A., Varati A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 LLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 LVKLPGVGRKTANVVVSVAFGVPAIAVDTHVERVSKRLGICRWKDSVLEVEKTLMRKVP- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Endonuclease III (EC 4.2.99.18) (DNA-(apurinic or apyrimidinic site)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosidase; Lyase; Iron-sulfur; 4Fe-45; Complete proteome.

METAL 189 189 1RON-SULFUR (4FE-45) (BY SIMILARITY).

METAL 196 196 IRON-SULFUR (4FE-45) (BY SIMILARITY).

METAL 199 199 IRON-SULFUR (4FE-45) (BY SIMILARITY).

METAL 205 205 IRON-SULFUR (4FE-45) (BY SIMILARITY).

SEQUENCE 219 AA; 25000 MW; C38C66DA7948BA40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
Hydrolase; Nuclease; Endonuclease; Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KEDWS------VTHHRLIFFGR-YHCKAQSPRCAECPL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.0068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64;
                                                                                                                                                                                                                                                                                                                                                   EMBL; L47709; AAB38457.1; -. EMBL; Z99115; CAB14150.1; -. EMBL, Z99115; CAB14150.1; -. Subtilist; BG10256; nth.
InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004036; EndoIII_HH.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003563; HHH_1.
Pfam; PF00730; HHH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00478; ENDO3c; 1.
FIGRFAMS; TIGR01083; nth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.2%;
                                                                                                                                                                                                                                                                                                                                         EMBL; U11289; AAA80005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          END3_RICPR
005956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loca]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            END3_RICPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- FUNCTION: HAS BOTH AN APURINIC AND/OR APYRIMIDINIC ENDONUCLEASE
ACTIVITY AND A DNA N-GLYCOSYLASE ACTIVITY. INCISES DAMAGED DNA AT
CYTOSINES, THYMINES AND GUANINES. ACTS ON A DAMAGED STRAND, 5'
FROM THE DAMAGED SITE (BY SIMILARITY).

--- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or
apyrimidinic site in DNA is broken by a beta-elimination reaction,
leaving a 3'-terminal unsaturated sugar and a product with a
terminal 5'-phosphate.

--- COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE
CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER
POSITIONING OF THE ENTYME ALONG THE DNA STRAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
Hydrolase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair; Glycosidase; Lyase; Iron-sulfur; 4Fe-45; Complete proteome.

METAL 187 : IRON-SULFUR (4FE-45) (BY SIMILARITY).

METAL 197 : IRON-SULFUR (4FE-45) (BY SIMILARITY).

METAL 203 : 203 : IRON-SULFUR (4FE-45) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersson S.G.E., Zomorodipour A., Andersson J.O., sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                     Andersson J.O., Andersson S.G.E.; "Genomic rearrangements during evolution of the obligate intraccellular parasite Rickettsia prowazekii as inferred from an analysis of 52015 bp nucleotide sequence."; Microbiology 143:2783-2795(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.2%; Score 63.5; DB 1; Length 212;
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 0.0079;
10; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A7FDA4F6033A6382 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR004035; EndoIII_FCL.
Interpro; IPR004035; EndoIII_HhH.
Interpro; IPR0034055; EndoIII_HhH.
Interpro; IPR003551; FeS_bind.
Interpro; IPR003583; HHH_1.
SMART; SM00478; ENDO35; 1.
SMART; SM00478; ENDO35; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-madrid E;
MEDLINE-99039499; PubMed-9823893;
                                                                                                                                                                                               STRAIN=Madrid E;
MEDLINE=97419517; Pubmed=9274032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ235273; CAA15174.1; -. HSSP; P20625; 2ABK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24174 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y11778; CAA72458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR01083; nth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 24.1:
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 396:133-140(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ä

_ _ _ _ _ _ _

NTH OR RP746

.yase)

1.

```
Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Medina N., Mellado R.P., Mizuno M., Moesil D., Nakal S., Noback M.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sadaie Y.,
A Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
A Settor., Scanlan E., Schleich S., Schrocter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P39788 bacillus su
005956 rickettsia
P17802 escherichia
P28325 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacteriopha
schizosacch
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mus musculu
caenorhabdi
schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methanobact
buchnera ap
arabis mosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   salmonella
homo sapien
methanobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rattus norv
saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treponema p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         saccharomyc
murine coro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 macaca mula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  schizosacch
                                                                                                                                 8, 2002, 19:24:14; Search time 8.26797 Seconds (without alignments) 1153.796 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       saimiri sci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muraenesox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 005556

P17802

P27802

P37802

P37802

P37803

P67803

P67803

P67803

P67803

P67803

P67803

P77803

P77803
                                                                                                                                                                                                                                                                                                                                                                                                                                                           112892
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                         112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTD_HUMAN
END3_THEMA
OGG1_RAT
OGG1_YEAST
OGG1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OGGI_METTH
YNNZ_YEAST
Y9K_BPP4
YDK9_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNR9_MOUSE
M3K5_MOUSE
CYTC_SAISC
END3_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETFA_HUMAN
ETFA_MOUSE
CUT1_CAEEL
MYH_SCHPO
YAOT_SCHPO
YAOS SEAST
RRPA_CYMJH
GTHB_MURCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTY_SALTY
OGG1_HUMAN
                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  END3_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTC_HUMAN
CYTC_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTH2_ANGAN
                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1066887777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.55  
5.57  
5.58  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5.59  
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.5
46.5
46.5
46.5
46.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                            OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                         Sednence:
                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                              on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
```

			45.5 45	6.6	457		YEBQ_ECOLI CYTN_HUMAN		P76269 P01037	escherichia homo sapien
		9	44.5 44.5	4.4.	249 327		YB4E_SCHPO		014359 Q9v3i8	schizosacch drosophila
		<b></b>	4 4	4.	438		GLGA_THECA		P58395	thermus cal
		10	۳	. m	151		PA2X_RAT		Q9qzt3	rattus norv
		41 42	4 4 4 4	ო. ო.	275 344		VA16_VACCV Y613_METJA		P16710 Q58030	vaccinia vi methanococc
		43 44	4 4 4 4	m m	377		VA16_VARV		P33841	variola vir
		45	44	. e.	486		GATB_AERPE		09yb79	aeropyrum p
							ALIGN	ALIGNMENTS		
	RESULT	olr 1								
.:••	i a s	ENDS_BACSU ID ENDS_BACSU	SACSU	STANDARD;	ARD;		PRT;	219 AA.		
	P. T.	01-FEE			., Created)	ate	(pa			
	D D	01-FEE 15-JUN	01-FEB-1995 ( 15-JUN-2002 (	(Rel. 31 (Rel. 41	31, Last 41, Last	t t	equence unnotatio	sequence update) annotation update)		
	DE	Probak	- 0	nucle	ase III (EC 4	, E	C 4.2.99	.18) (DNA-(apurinio	c or	
	O E	apyrın NTH OF	apyrimidinic NTH OR JOOB.	site)	yase)					
	SO	Bacil1	Bacillus subtilis	ilis.						
	88	Bacter	Bacteria; Firmicutes;	micutes		11	ales; Ba	Bacillales; Bacillaceae; Bacillus	vo	
	R C	[1]	axıD=14	, 62						
	RP	SEQUEN	SEQUENCE FROM N.A	N.A.						
	RC:	STRAIN	V=168;	i c	;	ľ	0			
	XX c	MEDLIF	VELUDZIV	JUES; PU	=pwed=	7/1	1426U;	40.40		
	¥ ¥	"Nucle	otide s	rokin F	of t	i e	Bacillus	bruand C., SOLOKIN A., Serior F., Enflich S.D.; "Nucleotide sequence of the Bacillus subtilis dnaD gene	 a	
	RL	Microk	iology	141:321	-322(	199	15).			
	RN	[2]								
	A S	SEQUE	SEQUENCE FROM	FROM N.A. 8 / Marburg						
	XX	MEDLIN	MEDLINE=96349105; PubMed=8760912	1105; Pu	bMed=	876	0912;			
	RA	Soroki	Sorokin A.V., Azevedo V.,	Azeved	lo V.,	20	mstein E	Zumstein E., Galleron N., Eh	Ehrlich S	S.D.,
	RA	Serror P.;	: P.; ance ana	lveie	+ +	ď.	o allina a	the Bacillus subtilis chromosome region	region	hotwoon
	RT	the se	the serA and kdg loci	kdq loc	i clo	ned	l in a ye	ast artificial chro	Smosome	
	RL	Micro	Microbiology	142:200	5-201	6(1	.696)			
	RN	[3]								
	д 2	SEQUEN	SEQUENCE FROM N.A.	N.A.						
	Z X	MEDLIN	VE=98044	033; Pu	-pwed=	938	14377:	SINGIN 108; MEDLINE=98044033; PubMed=9384377;		
	RA	Kunst	F., Oga	sawara	Z Z	osz	er I., A	lbertini A.M., Allo	oni G.,	
	RA	Azevec	30 V., E	Sertero	M.G.,	Be	ssieres	P., Bolotin A., Bo	rchert	S.,
	KA 4	Bronil	35 K., E	Soursier		Pra	ins A., B ຕາໄດ້ແຄ່ໄ	raun M., Brignell S	S.C., B	ron S.,
	RA	Choi	. K. C.	dani T.	) !	o, o	erton I.	F. Cummings N.J.	Daniel	R. A.
	RA	Denizo	ot F., D	evine K	Σ.	Dus	terhoft	Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., I	Emmerso	n P.T.,
	RA	Entian	K.D.,	Erringt	on J.	Ή.	abret C.	, Ferrari E., Foulo	ger D.,	
	RA PA	Fritz Chim e	C., Fuj	ita M.,	Fuji	ta	Y., Fuma	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Chim S. V., Glasor D. Coffoan A. Colichtly F.I. Grandi C.	alleron	`. Z
	R'A	Guiser	opi G.,	Guy B.J	, Ha	ם קמ	K., Haie	ch J., Harwood C.R.	ıı G., ., Hena	ut A.,

. В

THIS PAGE BLANK (USPTO)

	0;
	Gaps
	0;
CADHERIN 22. CADHERIN 23. CADHERIN 24. CADHERIN 25. CADHERIN 26. CADHERIN 26. CADHERIN 27. MISSING (IN ALLELE D1). I -> V (IN REF. 3). S -> G (IN REF. 3). I -> L (IN REF. 3). G -> S (IN REF. 3). G -> R (IN REF. 3). G -> S (IN REF. 3). G -> S (IN REF. 3). G -> S (IN REF. 3). C -> R (IN REF. 3). G -> S (IN REF. 3). FYEGO STATE CRC64;	
2374 2472 2481 2576 2586 2686 2695 2793 2804 2897 2927 3020 1131 1153 1070 1070 1490 1490 1636 1636 1636 1636 1636 2210 2220 2210 2289 2289 2286 2289 2286 2289 2286 2289 2286 2289 2286 2289 2386 3283 3383 3383	'at
FT REPEAT 2374 FT REPEAT 2481 FT REPEAT 2586 FT REPEAT 2695 FT REPEAT 2604 FT REPEAT 2927 FT CONFLICT 1070 FT CONFLICT 1490 FT CONFLICT 1692 FT CONFLICT 1692 FT CONFLICT 2229 FT CONFLICT 2229 FT CONFLICT 2239 FT CONFLICT 2289 FT CONFLICT 2289 FT CONFLICT 2862 FT CONFLICT 2863 F	Matches 7;

Qy Db

Search completed: November 8, 2002, 19:28:42 Job time : 40.2614 secs

```
Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3046
3067
58
130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1109
1213
1320
1440
1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1803
1907
2012
2122
2261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
           RRAPA
RAPA
RRAPA
R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., A Sutton G.G., Wortman J.R., Yandell M.D., Change M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D., RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Rayler R., Cadleu E., Center A., Chandra I., Rattis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Rayler B., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A., Loerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-EMBRYO;
MEDLINE-95324813; PubMed-7601355;
MEDLINE-95324813; PubMed-7601355;
Clark H.F., Brentrup D., Schneitz K., Bieber A., Goodman C., Noll M.;
Dachsous encodes a member of the cadherin superfamily that controls imaginal disc morphogenesis in Drosophila.";
Genes Dev. 9:1530-1542(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                       "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noll M.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA binding; Zinc-finger.
SEQUENCE 624 AA; 71971 MW; 39E9BD2838A9C8D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                        investigating biology.", Science 283:2018-2018(1998).
EMBL, 275552; CAA99942.1; -
Interpro; IPR000822; Znf_C2H2.
Ffam; PF00096; zf-C2H2; 1.
SMART; SM00355; ZnF_CZH2; 1.
PROSTIE; PS50157; ZINC_FINGER_C2H2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.3%; Score 37; DB 5;
64.3%; Pred. No. 23;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Last seque 01-JUN-2002 (TrEMBLrel. 21, Last annot DACHSOUS protein precursor (ADHERIN). DS OR CG17941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY; MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                   MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O24292 PRELIMINARY;
O24292; Q9VPS4;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 64.3
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 LRIEHDV--LPDVH 101
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                    SEQUENCE FROM N.A.
                                                         z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                         Lennard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
  ACCOORDING TO THE SECTION OF SECT
```

```
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rolek A., Gong F., Gorg N.S., Gelbart W.M., Glasser K., Androdek A., Gong F., Gorrell J.H., Gu Z., Gana P., Harris M., Harrey D., Heiman T.J., Hernandez J.R., Houck J., Houck J., Harris N.L., Harvey D., Heiman T.J., Wein M.-H., Ibegwam C., Jalai M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A., Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Martei B., McIntosh T.C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nelson R.A., Nixon K., Nusskern D.R., Pacleb J.M., Reinert K., Remington K., Sunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Suith T., Shen B.C., Scheeler F., Wang X., Shue B.C., Stapleton M., Strong R., Sun E., Spralling A.C., Stapleton M., Strong R., Sun E., Swith T., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Sheng X., Wen B.C., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao Q., Zhao X., When S., Where E.W., Wang S., Yao Q.A., Theng X., When S. Wang S., Wen S., Whilliams S.M., Woodege T., Worley K.C., Wu D., Yang S., Yao Q.A., Theng X., When S. Wang S., Wenter E., Wang S., Yao Q., A., Weinston S., Wenter E., Wang S., Yao Q., Zhao R., Whens E.W., Rubin G.M., Venter J.C.; Shu X., Smith H.O., Steinee 299, 2195, 2006, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: INVOLVED IN MORPHOGENESIS. MAY ALSO BE INVOLVED IN CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
-!- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC ECTODERM. IN LARVAE,
EXPRESSION IS RESTRICTED TO IMAGINAL DISKS AND BRAIN.
-!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT EMBRYOGENESIS WHERE IT
IS FIRST DETECTED DURING GASTRULATION. ALSO EXPRESSED IN LARVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00232; CADHERIN_1; 19.
PROSITE; PS50268; CADHERIN_2; 27.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
DACHSOUS PROTEIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND ADULTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 6.
CADHERIN 6.
CADHERIN 7.
CADHERIN 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CADHERIN 19.
CADHERIN 19.
CADHERIN 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CADHERIN 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CADHERIN 16.
CADHERIN 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CADHERIN 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CADHERIN 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CADHERIN 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CADHERIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    983
1100
1203
1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1431
1548
1665
1793
1899
2003
2146
2269
```

,; ;;

```
InterPro; IPR002637; Hamlp_like.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W04D2.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wamsley P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
6
                                                                              Query Match
                                                                                                                                                                                                                                                                                                      C55B7.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W04D2.4
                                                                                                                                                                                                                                        Q966MO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   023159;
                                                                                                                                                                                                                         0966M0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    023159
                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
  δ
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                      Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capela D., Barloy Hubber F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Backer A., Boutry M., Cadieu E., Dreano S., Gloux S., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizoblum mellioti strain 1021."; Brock St. Callbert F.; EMBL, ALS91783; CAC41811.1; -.
                           Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBL_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 16; Length 1540;
Pred. No. 35;
1; Mismatches 13; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02801; ketoacyl-synt_c; 1.
Pfam; PF00550; pp-binding; 1.
PROSITE; PS00075; ACP_DOMAIN; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
Phosphopantetheine; Transferase; Complete proteome.
SEQUENCE 1540 AA; 164209 MW; D7042CAAREB72375 CRC64;
                                                                             Murphy L., Harris D.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein R00374.
                                                                                                                                                                                                                                                                         "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011/2001).
EMBL, AL035480; CAB56627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 AA.
                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001227; Ac_transferase.
InterPro, IPR000794; Ketoacyl.synt.
InterPro, IPR003880; Ppantne_attach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=1021;
MEDLINE=21396507; PubMed=11481430;
                                                                                                                                           MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                     Piam; PFUU698; Acyl_transf; 1.
Pfam; PF00109; ketoacyl-synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              990 DHDVSTLHDLHNALRGVDNVLY 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * 112 EHXVXXLPDXHXXLXXXDXXXY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.48;
                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00698; Acyl_transf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 30.4.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
Mycobacterium leprae.
                                                                SEQUENCE FROM N.A.
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               Leproma; ML2356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q92SK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                           . 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 325;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-D...
Waterston.";
"Direct Submission.";
"Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006625; AAK68211.1;
"FOUTHINGE 325 AA; 37141 MW; 55EAA4186BC645C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of C. elegans cosmid C55B7.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
Pfam; PF01725; Hamlp_like; 1.
TIGRETMS: TIGR00042; Hamlp_like; 2.
Hypothetical protein; Complete proteome.
SEQUENCE 214 AA; 23109 MW; A282C7539C9BBCDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                           Score 37; DB 16;
Pred. No. 7.1;
                                                                                                                                                                                                    110 RTEHXVXXL----PDXHXXLXXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                  125 RTARFVSVLCLAWPDGHVELFRGEVEGYV--VWPP 157
                                                                                                                                                                                                                                                                                                                                                         325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 624 AA.
                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.3%; Score 37; DB
86.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 LRTEHXVXXLPDXHXXLXXXXXXX 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 LNTETLIEILPDGKLILNPRDASKY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein C55B7,11.
                                                                                                             6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01,
01,
20,
                                                                                                                             Local Similarity 31.4 hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel
01-DEC-2001 (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
```

ö

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9S384
Q9S384;
                                                                                                                                                                                                                                                                                                               049932
                                                                                                                                                                                                                                                                                                                                 049932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
Q9S384
                                                                                                                                                                                                                                                                                RESULT 10
Q49932
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
            RL
DR
DR
DR
SO
SO
                                                                                                                                                                                               ò
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Baxter E.G., Helt G., Nelson C.R., Malklos G.L.G.,
RA Ballew R.M., Baxter E.G., Helt G., Nelson C.R., Malklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Andrin D.,
RA Ballew R.M., Basu A., Butler H.-Galden E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cepblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gabart W.M., Glasser K.,
Glodek A., Gong F., Gorreil J.H., Gu Z., Guan P., Harris M.,
Harrish N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Hint S.M., Moy M., Murphy B., Murphy L., Murahy D.M., Nelson D.L.,
RA Heison D.R., Nelson K.S., Van S., Pollard J., Puri V., Resee M.G.,
RA Reinert K., Remington K., Saunders R.D. Skupski M.P., Smith T.,
Sher B.C., Spradling A.C., Stapheton M., Strong R., Sun E.,
Wung Z., Yan W., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Gliber S.M., Woodger T., Worler J.C.;
RA Gliber S.M., Woodger T., Worler J.C.;
RA Gliber S.M., Whood W., Strong R., Shing R.,
Rhomer S.M., Robong F.N., Robing S.M., Woodger T., Worler J.C.;
Rhomer S.M., Robong F.N., Robing S.M., Walley S.M., Walley S.M., Walley S.M., Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gentry-Weeks C.R., Keith J.M., Estay M.T., Pikis A.;
Gentry-Weeks C.R., Keith J.M., Estay M.T., Pikis A.;
"A resident plasmid of Enterococcus faecalis 418 contains multiple
IS1216v elements, aminoglycoside and lincosamide resistance genes, and
a putative ABC transporter gene with similarity to the Streptococcus
pneumoniae macrolide efflux pump gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 5; Length 1548; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 1548 AA: 174352 MW; 87D782E7B27E0EE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    935 PROTKTRFKLPTDLKTDHSVVKLPPKQENLPHFDVAAVL 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 PXXXXXXXXXXXXXRTEHXVXXLPDXHXXLXXXXXXXI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis (Streptococcus faecalis).
Plasmid pEF418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative spectinomycin adenyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 6.9%;
Best Local Similarity 28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003519; AAF49220:1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0014075; Ugt.
InterPro; IPR002495; GT_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q93CK3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          093CK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
```

```
ö
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Robison K., Smith D.R.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POTENTIALLY INVOLVED IN SOME INTERNEDIATE STEPS FOR THE SYNTHESIS OF A POLYKETIDE MOLECULE WHICH MAY BE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multifunctional enzyme, Repeat; Ligase.
ACT_SITE 204 204 BETA-RETOACYL SYNTHASE (BY SIMILARITY).
ACT_SITE 651 ACT_TRANSFERASES (BY SIMILARITY).
SEQUENCE 1446 AA; 153871 MW; 5D23A2E5E6155F4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium leprae.
Bacteria, Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SIMILARITY: TO FATTY ACID SYNTHASE (FAS).
-i- SIMILARITY: TO ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT
BINDING OF AMP TO THEIR SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: CONTAINS THREE COVALENTLY BOUND PHOSPHOPANTETHEINES
                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1446;
                                                                                                                                                                                                           6.4%; Score 38; DB 2; Length 242; 34.6%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                                                                                                           Indels
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF408195; AAL05551.1; ...
InterPro; IPR002934; NTP_transf.
Pfam; PF01909; NTP_transf_2; 1.
Plasmid; Transferase.
SEQUENCE 242 AA; 27360 MW; 503AlE863E48B90C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, 000023; AAA17356.1; -.
InterPro: IPR00122; Ac_transferase.
InterPro: IPR00194; Ketoacyl-synt.
Pfam; PF00109; Ketoacyl-synt; 1.
Pfam; PF00109; BKETOACYL_SYNTHASE; 1.
Hypothetical protein; Transferase; Acyltransferase; Antibiotic blosynthesis; NADP; Phosphopantetheine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1540 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                             Pred. No. 4.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative polyketide synthase PKSC (PKS).
PKSC OR L518_F1_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.4%; Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                     109 LRTEHXVXXLPDXHXXLXXXDXXXYL 134
                                                                                                                                                                                                                                                                                                                                                                      990 DHDVSTLHDLHNALRGVDNVLY 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 EHXVXXLPDXHXXLXXXDXXXY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative polyketide synthase.
ML2356 OR MLCB12.01C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.48;
                                                                                                                                                                                                                                                Best Local Similarity 34.69
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 36.4 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECONDARY METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996
```

 $\sim$ 

ö

```
SEQUENCE
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         095028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9VVT7
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
    RT
RL
DR
DR
FT
FT
SO
                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1094 KNISQLRTEHRVYELPDEHPLLAQLEKREPDDPCSYLLAIWTP-GETADSIQPSVSTC-- 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 6.1 Kba protein (Fragment).
Narcissus pseudonarcissus (Daffodil).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Weichselgartner M., Fartmann B., Granderath K., Dauner D., Herzl A.,
Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Δ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bevan M., Weichselgartner M., Fartmann B., Granderath K.,
Herzl A., Neumann S., Hohelsel J., Jesse T., Heijnen L., V
Mewes H.W., Mayar K., Schueller C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AL021961; CAA17566.1;

EMBL, AL1051964; CAB0123.1;

InterPro; IPR003265; Endo_3c.

InterPro; IPR003651; Fes_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al protein.
917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 KXXXXLRTEHXVXXLPDXHXXL-----XXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYYNRLRTEHVVYVLPDNHELLHDFERRKLDDPSPYLLAIWQP 878
                                                                                                                                                                                                                                                                            ol-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Hypothetical 106.3 kDa protein. SEAR23.180 OR AM4G34060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.1%; Score 77; DB 10; 44.2%; Pred. No. 2.5e-08;
                                                                                                             1151 -IFQANGMLCDEETCFSCNSIKETRSQIVRGTIL 1183
                                                                                                                                                                                                                                AA
                                                                 53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CV. DUTCH MASTER; TISSUE=TEPAL;
Hunter D.A., Reid M.S.;
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 44.2
nes 19; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00730; HhH-GPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Narcissus.
NCBI_TaxID=39639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90WV8Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      836 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
98 WWG
1D 08 WW
AC 08 WW
DT 01 - WM
DT 01 - MM
DT 01 - MM
DE HYPO1
OS NATC!
OC BURAI
OC SPERT
OC NATC!
OC NATC!
OC NATC!
OC SPERT
OC NATC!
OC NATC!
OC SPERT
OC NATC!
                                                                                                                                                                                                      049498
                                                                                                           q
                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
```

```
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Champe M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (COT-201) to the EMBL/GenBank/DDBJ databases.

EMBL, AY058353, AAL136821.

FIYBase; FBGRO014075, UGt.

SEQUENCE 1064 AA; 119309 MW; 40A569D1A68513CD CRC64;
"Identification of genes associated with perianth senescence in daffodil (Narcissus pseudonarcissus L. 'Dutch Master')."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF40221; AAL6934.1; -...
                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 1064;
                                                                                                                                                                                                                                              Score 47; DB 10; Length 53;
Pred. No. 0.0083;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                1FDE4BC8CED27346 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                3 IFKGLTTEGIQHCFWRGFVCVRGFDRMMRAPKPLFARLHFPASK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 PXXXXXXXXXXXXIRTEHXVXXLPDXHXXLXXXDXXXYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                935 PRQTKTRFKLPTDLKTDHSVVKLPPKQENLPHFDVAAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1064 AA
                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1548 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                    8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.9%;
28.2%;
                                                                                                                                                                                                 53 AA; 6138 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAX-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 28.2
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UGT OR CG6850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UGT protein.
UGT OR CG6850.
```

~

<u>ب</u>

Length 1309:

09FT02

RESULT 2 Q9FTQ2

g

g ò g

õ

```
STRAIN-CV. COLUMNIA;
MEDLINE=20083487; Pubbed=10617197;
Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S. Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Evili C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J. Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.,
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                          1166 ALFESNNTLCNENKCFQCNKTREEESQTVRGTILIPCRTAMRGGFPLNGTYFQTNEVFAD 1225
                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                             Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E. Bowman C.L., White O., Wierman W.C., Fraser C.M.; "Arabidopsis, thaliana chromosome III BAC T22K18 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDSSINPIDVPTELIWDLKRRVAYLGSSVSSICKGLSVEAIKYNFQEG 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00730; HhH-GPD; I.
SMART; SM00478; ENDO3c; I.
SMART; SM00525; FES; I.
SEQUENCE 1309 AA; 148451 MW; 3B21E4439BA4A673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDB6C9EE94DDF67 CRC64;
                                                                           Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AC010927, ARC04422.1; -. InterPro; IPR003265; Endo.3c. InterPro; IPR003661; FeS_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                             18.4%; Score 108.5; DB 10; 25.0%; Pred. No. 2.3e-15; iive 0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 91; DB 10; 29.8%; Pred. No. 2.1e-11; ive 0; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC006919; AAD24633.1; -. InterPro; IPR003651; FeS_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similaricy
hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1207 AA;
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        At2936490 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eurosids II; Bra
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00525;
SEQUENCE 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001
                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AT2G36490
                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901360
                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
Q9SJQ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ë,
95 -GGKASGKMCFDETCSECNSLREANSQTVRGTLLIPCRTAMRGSFPLNGTYFQVNELFAD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 KNVSRLRTEHQVYELPDSHPLLEGFNQREPDDPCPYLLSIWTP-GETAQSTDAPKSVC-- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 -NSQENGELCASNTCFSCNSIREAQAQKVRGTLLIPCRTAMRGSFPLNGTYFQVNEVFAD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 HDSSRNPIDVPRSWIWNLPRRTVYFGTSIPTIFKGLTTEEIQHCFWRGFVCVRGFDRTSR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                     154 HESSLKPIDVPRDWIWDLPRRTVYRGTSVTSIFRGLSTEQIQFCFWKGFVCVRGFEQKTR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 KXXXXLRTEHXVXXLPDXHXXLXX-----XDXXXYLLXIWXPXXXXXXXXXXXXXXXX 157
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0665D10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.6%; Score 145; DB 10; Length 274; 26.2%; Pred. No. 2e-24; 1ve 0; Mismatches 134; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002861; BAB16489.1; -- SEQUENCE 274 AA; 30951 MW; D7C826BD3982592D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ol-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T2X18.18 protein.
                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                   274 AA
                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 16, C
(TrEMBLrel. 16, I
(TrEMBLrel. 16, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                 1 1 11 11 214 APRPLMARLHFPASK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 XPXXLXXXLHXXXSK 292
                                                                                                                    278 XPXXLXXXLHXXXSK 292
                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 APRPLYARLHFPASK 257
                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLre)
01-MAR-2001 (TrEMBLre)
P0665D10.14 protein.
P0665D10.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                       01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

Matches

qq

ð

셤

ò

g

ò g

ò

RESULT 3 Q9SR66

a,

Gaps

10;

Q8r1f7 mus musculu

Opth9 xenopus lae Optm8 pseudomonas Oguvo alternaria 005516 bacillus su 093955 yarrowia li 0873K1 yersinia pe Oppi45 campylobact 097v74 sulfolobus 099km7 mus musculu 099km7 mus masculu 051815 bacillus su

092200 mus musculu 09k164 neisseria m 09jsr4 neisseria m 09jsr4 neisseria m 09fs10 aculobacter 00f561 bacillus su 09fs2 bacudomonas 09rt59 deinococcus 08ycz9 brucella me 08szx4 drosophila 09vc29 drosophila 09vc29 drosophila

09arc4 vallisneria 09k3x3 streptomyce 09arp2 saccharopol 09a7u8 caulobacter 09nvn5 homo sapien 096cg1 homo sapien

Sednence:

Run on:

Searched:

```
ALIGNMENTS
                  QQUVN5
093955
0823K1
092045
09P045
09P045
09P046
099K07
Q8R1F7
Q9PTH9
Q9HZM8
                                                                                                                                                                   Q9VCZ9
Q9ABP5
                                                                                                                                                              Q8SZX4
 111
113
116
110
110
110
                                                                                                        4
111
116
116
116
116
 091267 arabidopsis
09ftq2 oryza sativ
09sr66 arabidopsis
09sr96 arabidopsis
049498 arabidopsis
049408 arabidopsis
0495028 drosophila
095028 drosophila
09363 enterococcu
049932 mycobacteri
095384 mycobacteri
095384 mycobacteri
092849 caenorhabdi
023159 caenorhabdi
023159 caenorhabdi
023159 caenorhabdi
023159 caenorhabdi
                                         8, 2002, 19:24:15 ; Search time 36.2614 Seconds (without alignments) 1659.222 Million cell updates/sec
                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                Description
                                                                                                                         671580
     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                           671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                      Q9LZ67
Q9FTQ2
Q9STR66
Q9SJQ6
Q49498
Q8VWU6
Q95U28
Q99VT7
Q93CK3
Q993SK4
Q993SK4
                                                                                                                                                                                 sp_archea:*
sp_archea:*
sp_fungi:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_plant:*
sp_vodent:*
sp_vodent:*
sp_virus:*
sp_vurtebrate:*
                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                       sp_archeap
                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                              SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                       234
274
1309
1207
917
917
1064
11548
1540
1540
325
624
325
624
339
                                          November
                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                          Score
```

Database

023159 024292 029807

0M9960

1122220 1122220 1022220

Result Š. THIS PAGE BLANK (USPTO)

```
The invention relates to human nucleic acids (AAI57798-AAI61369) and
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
immunosuppressant and cytostatic activity. The polynuclectides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral nervous
containsed neuropathies and central nervous system diseases, auch as
localised neuropathies and central nervous system diseases, auch as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
tulisation of the activities such as: Immune system suppression,
Activin/inhibin activity, chemotactic/chemokineic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemias and
c.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
specification.
                                                                                                                                                                                                         Example 2; SEQ ID NO 6504; 10078pp; English.
\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}
```

279 AA; Sequence

ö Gaps 0; Score 42; DB 22; Length 279; Pred. No. 32; 7; Indels 3; Mismatches 7; Indels 7; Indels Query Match 15.3%; Soc Best Local Similarity 41.2%; Pre Matches 7; Conservative 3;

49 QGXRXFXXWKGSVVDSV 65

ŏ qq

Search completed: November 8, 2002, 19:25:54 Job time : 16.9706 secs

```
Wang
                                                                                                                                                                                                                                                                               09
                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                           AAM41573
                                                                                                                                                                                                                                                                                                                                                 a
    00000000000000000000
                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                     ö
In gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin, inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constructions.
                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ren F, Wang D;
Zhang J;
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                     0
                                                                                                                                                                               DB 22; Length 232;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qian XB,
Yang Y,
                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO 2933; 10078pp; English
                                                                                                                                                                                         Pred. No. 25; Mismatches
                                                                                                                                                                                Score 42;
                                                                                                                                                                                                                                                                                                     - AAM39788 standard; Protein; 258 AA.
                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 2933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                               15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0488725.
2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0598042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0620312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0653450
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                          QGXRXFXXWKGSVVDSV 65
                                                                                                                                                                                                                                               34 EGDEPITOWKGTVLDQV 50
                                                                                                                                                                                         Best_Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                          232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI58944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukaemia.
                                                                                                                                                                                                                                                                                                                           AAM39788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao QA,
                                                                                                                                                           Sequence
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                           AAM39788
                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                           ò
```

ň

```
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activities such as Immune system 'suppression' Activities such as Immune system 'suppression' Activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ر
ا
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren F,
Zhang J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.3%; Score 42; DB 22; Length 258; 41.2%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nen R, Ma Y, (
{u C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       χυ C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM41573 standard; Protein; 279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 6504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0488725.
2000US-0552317.
2000US-0598042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 QGXRXFXXWKGSVVDSV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGDEPITOWKGTVLDOV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                    258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAI60729
                                                                                                                                                                                                                                                                                                                                     C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang J, I
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM41573;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

~

```
Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the cares. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies spolypeptides may be used as antigens in the production of antibodies condequate expression and activity of P. acnes polypeptides and convenient of downrequiate expression and activity of P. acnes polypeptides and categories. These antibodies may also be used as character treat P. acnes infections. The acnes proteins as a canes proteins and activity of P. acnes presence, for example, by acres in a canes proteins and activity of P. acnes presence, for example, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme linked immunosorbent assay (ELLSA).
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a polypeptide that is critical for the survival and growth of Candida albicans. The C. albicans nucleic acid molecules encoding the polypeptides of the invention may be used as probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in the
in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viaene JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida albicans infection; growth; survival; medicament; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Backer MD, Luyten WHML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Essential polypeptides isolated from Candida albicans, treatment of diseases caused by C.albicans, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of diseases caused by C.albicans, especially immunocompromised subjects, e.g., AIDS patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vulvovaginitis; immunocompromised patient; treat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 2
Pred. No. 36;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 WKACLAEGVLCLFLTANDGTMAS----YLAESFP 366
      Example 1; SEQ ID No 3451; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans polypeptide sequence # 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 WKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 59-60; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY95051 standard; Protein; 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98EP-0310694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0017796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contreras RH, Nelissen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 32.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-258614/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP982401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Logghe MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY95051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY95051
\overset{\mathsf{A}}{\times}\overset{\mathsf{A}}{\times} \overset{\mathsf{A}}{\circ} \overset{\mathsf{A}}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

1;

```
ö
primers for detecting homologous nucleic acid molecule sequences. The polypeptides and nucleic acid molecules and compounds identified as selectively modulating the expression of the polypeptides, may be used as medicaments or for the preparation of a medicament to treat C.albicans associated diseases, especially in AIDS patients and to treat vulvovaginitis in otherwise healthy females. The use of the polypeptides and polynucleotide sequences to treat C.albicans associated diseases has fewer side effects and less toxicity than previously used methods such as the use of amphotericin. This method is therefore especially suitable for immunocompromised patients, such as AIDS patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang D;
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peripheral nervous system neuropathy; central nervous system; CNS; Alzheimer's, Parkinson's disease, Huntington's disease, haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ren F, W
Zhang J;
                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                        DB 21; Length 466; 39;
                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ten R, Ma Y, (C, Xue AJ, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 2932; 10078pp; English.
                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       central nervous system injuries
                                                                                                                                                                                                Score 43;
                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen R,
                                                                                                                                                                                                                                                                                                                                                             AAM39787 standard; Protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   χu c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 2932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Asundi V,
Wang Z, Wehrman T,
                                                                                                                                                                                               15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0552317.
2000US-0598042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0620312.
2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0662191
2000US-0693036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-2001 (first entry)
                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                         57 WKGSVVDSVXGV 68
                                                                                                                                                                                                                                                                                      79 WEGSVLDPIEGI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-442253/47.
                                                                                                                                                                                                            Sest Local Similarity
                                                                                                                                                                   466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAI58943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                          AAM39787;
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             API;
                                                                                                                                                                                                                                                                                                                                              AAM39787
                                                                                                                                                                                                                                                                                                                                                               οp
                                                                                                                                                                                                                                                          ò
```

9

```
Claim 6; SEQ ID No 992; 192pp; French.
   related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS59516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU42256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU42256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                            The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA01910) that exhibit activity elating to cytokine. cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy, The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis requiating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchrleser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquer F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                               Claim 20; SEQ ID NO 18456; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 22; Length 106;
Pred. No. 4.2;
2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB48287 standard; Protein; 434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 MXXXQGXRXFXXWKGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 MLGVQGASRFGVWGGAVSWSIDGAVL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.0%;
ilarity 38.5%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-2000; 2000FR-0004629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-010914/01.
WPI; 2001-514838/56.
N-PSDB; AAI84495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2001
                                                                                            disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB48287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rose M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
```

QQ ð

```
The present invention relates to the genome sequence of Listeria monocytogenes EGD-6 (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes. related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO. at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalnitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 23; Length 434;
Pred. No. 36;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes immunogenic protein #3152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW, Persing DH, Mitcham JL, Wang SS,
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU42256 standard; Protein; 436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.6%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 5/...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 VDTIGGWFLTQNYE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 VDSVXGVFLTQNXD 75
```

ó

```
WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA004564
 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyellits), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaries. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention polypeptides may be used as antigens in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                          Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                    downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                               17.5%; Score 48; DB 22; Length 235; 32.0%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashi K,
                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                 Example 1; SEQ ID No 7822; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein sequence SEQ ID NO:12081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB93159 standard; Protein; 882 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 QGXRXFXXWKGSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 EGAKTFVSWMGSIVPLVLMLLIAMN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000EP-0116126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                          treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HELI-) HELIX RES INST.
           WPI: 2001-616774/71
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       235 AA;
                        N-PSDB; AAS59534,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ota T, Is
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB93159;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB93159
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence 1s selected from those defined in the specification: The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH0316 to AAH13628 and AAH18633 to AAH18632 cepresent human cDNA sequences; AAB9446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AABB5893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchie; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                 Claim 8; SEQ ID 12081; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.7%; Score 46; DB
33.3%; Pred. No. 24;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 RXFXXWKGSVVDSVXGVFLTQNXDXXS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 18456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO04564 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          882 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO04564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
```

Disclosure; Page 75; 109pp; English.

```
complement encoding a polypeptide having a sequence at least 40%

identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B

or Cor their combinations. Also included are an expression

cassette comprising the polynuclectide or comprising a heterologous

DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated

cassette comprising an exogenous polynucleotide

DMT 6' flanking sequence, DMT 3' flanking sequence or an 5' untranslated

careding a DMT-like protein. The expression cassette is

cassette flance and atransgenic plant comprising a

cuseful for modulating transcription. The method comprises introducing

the cassette into a host cell with modulated transcription, where

the protein is capable of exhibiting at least one of the following

cross, and selecting a host cell with modulated transcription of the

protein is capable of exhibiting at least one of the following

biological activities, which include enhanced expression of the

protein in a plant results in a delay in flowering time, introduction of

chromosomal DNA in the cell, reduction of expression of the protein in a

plant results in enhanced endosperm development and expression of the

chromosomal DNA in the cell, reduction of expression of the protein in a nathadopsis leaf results in expression of the DNA in the cell, reduction of expression of the Protein in a plant results in enhanced endosperm development and expression of the

CROPETER is related to 5-methyloytosine glycosylases and regulates

changes and selecting a pure of the construction of the present expression of the protein and expression of the modulates

changes and selecting a useful for detecting a nucleic acid in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; Length 1952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 162.5; DB 23; Length
Pred. No. 2.7e-20;
Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 926 RFSPWKGSVVDSVVGVFLTQNVSDHLSSSAFMALAAKFP 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU72741 standard; Protein; 1114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis DMT4 (1DMT4) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fischer RL, Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis Thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1952 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Bëst Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS96694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU72741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88888888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
5
                                                                                                                                                                                                                                                           Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bolynucleotide encoding a by Talke protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of plant results in enhanced endosperm development and expression of the protein in an Arabidopsis leaf results in expression of the MEDEA gene protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylation. The present transcription of target genes by demethylation. The present
                                                                                                               The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (EBMETER, previously known as ATROPOS (ATR)) Domain A, Bo or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint, central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes immunogenic protein #7523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 162; DB 23;
Pred. No. 1.7e-20;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L, Wang SS,
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Persing DH, Mitcham JL,
e J, Zhang Y, Jen S, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU46627 standard; Protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-199047P.
2000US-208841P.
2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.98;
43.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2000;
02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU46627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \overset{\circ}{\otimes} \times \overset{\circ}{\otimes} \overset{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

Sat Nov

9 13:04:22 2002

```
region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgentc plant comprising a concoling a DMT-like protein and a transgentc plant comprises of polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of their protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide to S-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising a sequence or C -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DWT (DEMETER, previously known as ATROPOS (ATR)) Domain A, or C or their combinations. Also included are an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    697 KVDIDDETTRIWNLIMGKGDEKEGDEEKDKKKEKWWEEERRVFRGRADSFIARMHLVQGD 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KVXXDXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXERXXFXXXXXXXIXRMXXXQGX 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                             Length 1729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide that control plant development having a specific homology to DEMETER domains A,B
                                                                                                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                                                                                                                                                                       59.6%; Score 164; DB 23; ilarity 43.0%; Pred. No. 1.3e-20; Conservative 0; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 67; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU72737 standard; Protein; 1413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis DMT2 (1DMT2) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi Y, Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2001; 2001WO-US13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis Thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                        1729 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS96692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU72737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU72737
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

æ

```
3
                                                                                     polynucleotide encoding a bwr-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results to modulation of methylation of chromosomal DNA in the call, reduction of expression of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylation, the present transcription of target genes by demethylation. The present
cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXXERXXFXXRXXXXXQGXR 52
                                                                                                                                                                                                                                                                                                                                                                                                             Score 163.5; DB 23; Length 1413;
Pred. No. 1.2e-20;
0; Mismatches 47; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okamuro JK,
                                                                                                                                                                                                                                                                                                                                            sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 79-80; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU72743 standard; Protein; 1952 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                               59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                 3est Local Similarity 43.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                              1413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice DMT1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS96695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU72743;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
AAU72743
 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
```

οy g a

```
WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU72736;
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
AAU72736
                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                           ōλ
                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% indentical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included as an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is
                               The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                                                                                                                                                                                                                                                   497 KVOLDPETSRVWKLLMSSIDCDGVDGSDEEKRKWWEEERNMFHGRANSFIARMRVVQGNR 556
                                                                                                                                                                                                                                                                                                      DB 23; Length 1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Demeter: DMT: Atropos; ATR: 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tatarinova TV;
SEQ ID NO 1471; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                         Score 166.5; DB 23;
Pred. No. 3.1e-21;
...-+rhes 47;
                                                                                                                                                                                                                                                                                                                                                                                        53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 71; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU72739 standard; Protein; 1332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis DMT3 (1DMT3) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Σ
                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                     60.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-2001; 2001WO-US13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fischer RL, Choi Y,
                                                                                                                                                                     useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis Thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-055307/07.
                                                                                                                                                                                                    1309 AA;
                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS96693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2001.
                                                                                                                                                                                                                                                                        43;
 Claim 5;
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU72739;
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
                                                                                                                                                                                                                                                                                                                                                                        ٥٧ ،
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ø
                                                                                                                                                                protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates sequence represents a DMT-like protein. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, E or C or their combinations. Also included are an expression assette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT S' flanking sequence, DMT 3' flanking sequence or an 5' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 KVQLDPETSRVWKLLMSSIDCDGVDGSDEEKRKWWEEERNMFHGRANSFIARMRVVQGNR 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KVXXDXXTXXXWXXLXXXXDXXXXXXXX -----XXERXXFXXFXXXXXIXXMXXXQGXR 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 166.5; DB 2., 3.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 54-55; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU72736 standard; Protein; 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis Demeter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS96686, AAS96689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis Thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-055307/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
```

```
Herbicidally activ
Arabidopsis DMT3 (
Arabidopsis Demete
Arabidopsis DMT2 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice DMT1 protein.
Arabidopsis DMT4 (
                                                                                                                                                 (without alignments)
858.415 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                         8, 2002, 19:24:08 ; Search time 13.9706 Seconds
                                                                                                                                                                                                                             275
1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseg/genesegp-embl/AA1982.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1983.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/genesegp-emb1/AA2000.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseg/genesegp-embl/AA1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gcgdata/geneseg/genesegp-embl/AA2001.
                                                                                                                                                                                                                                                                                                                                                                                                    908470
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB92260
AAU72739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU72737
AAU72743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU72741
AAU46627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU72736
                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                П
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35553
                                                                                                                                                                                                         US-09-840-743-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1413
1952
11114
235
882
106
434
                                                                                                                           November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166.5
166.5
164
163.5
162.5
                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٠
ي
```

Propionibacter Candida albica Human polypept Human polypept Human polypept	Human proi Pristanoy Amino acid Novel hum Novel hum Novel hum Human int Human 5' I Berbicida' Streptocoo Streptocoo Streptocoo Streptocoo Streptocoo Streptocoo Streptocoo Human 5' I Human FLA Mouse FLA Muxine DED Human DEDI Human DEDI Human proi Human proi Human proi Human proi Human proi Human proi Human proi	Human Human Human 4 .
AAU42256 AAY95051 AAM39787 AAM39786 AAM41573	AAB93450 AAB93450 AAW483093 AAW4830353 ABG10353 ABB97191 AAY11870 ABB92345 ABP28344 AAY51682 AAW90108 AAW90108 AAW90108 AAW90108 AAW90108 AAW910396 AAK51022 AAW933385 AAK51023 AAK51023 AAK51023 AAK51023 AAK51023 AAK51023	
555555555555555555555555555555555555555	22222222222222222222222222222222222222	222
772303	370 370 371 371 371 371 371 371 371 371 371 371	000
	uuuuuuuuuuuuuuuuuu www.aaaaaaaaaaaaaaaaa	4 4 4
	44 444 . 4444 44444 4444	
117 113 114 115	7860108888888888888888888888888888888888	43. 44 45

## ALIGNMENTS

RESULT 1

Herbicidally active polypeptide SEQ ID NO 1471. Herbicidal; plant; agriculture; herbicide. ABB92260 standard; Protein; 1309 AA. 28-AUG-2001; 2001WO-EP09892. 28-AUG-2001; 2001WO-EP09892 31-MAY-2002 (first entry) Weidler M; Arabidopsis thaliana (FARB ) BAYER AG. WO200210210-A2. 07-FEB-2002 Tietjen K, ABB92260; **ABB92260** 

WPI; 2002-269010/31.

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms

Human protein sequ Human polypeptide

AAB93159 AAO04564 ABB48287

Propionibacterium

Listeria monocytog

```
610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 GXRXFXXWKGSV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDED TO BOX 980

STREET: P.O. Box 980

STREET: PAGE BOX 980

STATE: PAGE BOX 980

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: STATEM: DOX 900

COMPUTER: STATEM: DOX 900

SOFTWARRE: PAGE FORM:
APPLICATION NUMBER: US/09/240,410

FILING DATE: 20-JAN-1999

APPLICATION NUMBER: UX APPLICATION NO. 98300694.1

FILING DATE: 20-JAN-1999

ATTORNEY/AGENT INFORMATION:
NAME: PESTIA, PAUL F
NECTEMBATION NUMBER: DATE APPLICATION NO. 98300694.1

FILING DATE: 30-JAN-1998

ATTORNEY/AGENT INFORMATION:
NAME: PESTIA, PAUL F
NECTEMBATION NUMBER: DATE APPLICATION NO. 98300694.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 38; DB 4; Length 634; 58.3%; Pred. No. 1.6e+02; ative 0; Mismatches 5; Indels
                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.30

SUBTRANT ON DATE: March 11, 1998

CLASSIFICATION INDER: US/09/041,236

FILING DATE: March 11, 1998

CLASSIFICATION: 514

ATTORNEY FAGENT INFORMATION:

NAME: OSMAN, RICHARD A

RECISTRATION NUMBER: SEL198-001

TELEPHONE: (650) 343-4341

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 343-4342

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 634 amino acids

TYPE: amino acids

TYPE: MINDER: Linear

ATORIGHE WARE INDER: ACIDE OF THE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-240-410-2
Sequence 2, Application US/09240410
Fatent No. 6197544
GENERAL INFORMATION:
APPLICANT: MICHALOVICH, DAVID
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 23,031
REFERENCE/ZDOCKET NUMBER: GP-30039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.8
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-041-236-2
CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALIFORNIA: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 GXRXFXXWKGSV 61
                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
```

Garner, Ian

GENERAL INFORMATION:

```
Sequence 2, Application US/09041236
Fatent No. 6225285
GENERAL INFORMATION:
APPLICANT: Luo, Yuling
APPLICANT: Alomei, Xu
TITLE OF INVENTION: Semaphorin K1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 2;
Pred. No. 37;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    E: FISH & RICHARDSON P.C. 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09010/010001
                                                                            Sequence 33, Application US/08602359A Patent No. 5942430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          February 16, 1996
                                                                                                                                                             APPLICANT: MURPHY, Dennis
APPLICANT: REID, John
APPLICANT: MAFFIA, Anthony
APPLICANT: SWANSON, Ronald V.
APPLICANT: SWANSON, Ronald V.
APPLICANT: WARREN, Patrick V.
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 GXRXFXXW---KGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 GLRNLYSWSRVKGSLIISM-GVFL 94
                                                                                                                    GENERAL INFORMATION:
APPLICANT: ROBERTSON, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 184 AMINO ACIDS
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 13.8 Best Local Similarity 45.8 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: PROTEIN US-08-602-359A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             STREET: 422.
CITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: FE CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92037
                                   RESULT 13
US-08-602-359A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-041-236-2
                                                                                                       ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 317, Application US/09620412C

Patent No. 6448234

GENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

SEQ ID NO 317

LENGTH: 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 491;
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.2%; Score 39; DB 4; Length 646; Best Local Similarity 27.0%; Pred. No. 1.1e+02; Matches 10; Conservative 4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Indels
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/206,176
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 RXXXFIXRMXXXQGXRXFXXWKGSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 1
Pred. No. 78;
1; Mismatches
                                                                                                                                                               ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.28;
47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 WKGDKVKAHYGGFTVON 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.2
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 WKGSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 206-548-2329 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-206-176-4
                                                                                                                                                                                   STREET: 4225 F
                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                              STATE: WA
COUNTRY: US.
ZIP: 98105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-620-412C-317
```

δ Ω

```
326 RTLAFINNMSGDCGGAISADTQISITDTVKGILFENN 362
```

```
2,
            Gaps
            ٠.
Length 184;
           Indels
```

```
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-206-176-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-213-053-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09276993

Patent No. 6207801

GENERAL INFORMATION:
APPLICANT: Alnemi, Emad S.
APPLICANT: Alnemi, Emad S.
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF TITLE OF INVENTION: Of MAKING THE SAME, AND COMPOSITIONS FOR AND METHODS TITLE OF INVENTION: Of MAKING THE SAME NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOOGCOCK, Washburn, Kurtz, Macklewicz & No. 6207801ris
                                                                                            APPLICANT: Alnemil, Emad S.
APPLICANT: Fernandez-Alnemil, Teresa
APPLICANT: Fernandez-Alnemil, Teresa
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCES: 17
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.5%; Score 40; DB 4; Length 318; 33.3%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ed. No. 31;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: WINDOWS
SOFTWARE: WORDERfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
                                     Sequence 4, Application US/09276993
Patent No. 6207801
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 229
REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: ||:::: ||:| : 260 WRDYINGSLLEALKGVFITDS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.5
Best Local Similarity 33.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-09-276-993-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                  ΡA
                                                                                                                                                                                                                                                                                                              STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-276-993-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
GENERAL INFORMATION:

APPLICANT: AUDONNET. Jean-Christophe
APPLICANT: AUDONNET. Jean-Christophe
APPLICANT: AUDONNET. Jean-Christophe
TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
TITLE OF INVENTION: PARAINELUENZA 2 VIRUS
FILE REFERENCE: 454313-220
CURRENT APPLICATION NUMBER: US/09/213,053
CURRENT FILING DATE: 1996-06-27
EARLIER PILING DATE: 1996-06-27
EARLIER PILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 318,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 4
Pred. No. 31;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.2%; Score 39; DB 36.8%; Pred. No. 61; Live 4; Mismatches
                                       OPERATING SYSTEM: WINLOWL
SOFTWARE: WORDERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, MAIK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEFRON (215) 568-3100
TELEFRY: 318 anino acids
TENGTH: 318 anino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/08206176
; Patent No. 5639940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09213053 Patent No. 6159477
: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
14.5%;
Best Local Similarity 33.3%;
Matches 7; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Canine herpesvirus
US-09-213-053-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 RXFXXWKGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 RIWKTWRNSIKDNVCGEIL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.2
Best Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-276-993-6
                        COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: WORDPER
```

Gaps

4;

```
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: GAND-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                   Score 40; DB 3; Length 318;
Pred. No. 31;
8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ore 40; DB 3;
ed. No. 31;
Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-109-273-6; Sequence 6, Application US/09109273; Patent No. 6063760
                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJI
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                                                           260 WRDYINGSLLEALKGVFITDS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 WRDYINGSLLEALKGVFITDS 280
                                                                                                                                                                                                                                                                                      57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                     14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 WK----GSVVDSVXGVFLTQN 73
                TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: alinear
  (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.58;
                                                                                                                                                                                Query Match
Best Local Similarity 33.35,
-has 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                       ; MOLECULE TYPE: protein US-09-109-273-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-09-109-273-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΡA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alnemil, Emad S.
APPLICANT: Fernandez-Alnemil, Teresa
TITLE OF INVENTION: TEADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.5%; Score 40; DB 3; Length 318; 33.3%; Pred. No. 31; Live 8; Mismatches 2; Indels
One Liberty Place, 46th floor
                                                                                                                                                                            SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/109,273 FILING DATE:
                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA: MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR ESO ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acids
                                                 COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/859,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09109273
Patent No. 6063760
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.5
Best Local Similarity 33.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein US-08-859-167-6
                  Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Phil
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-109-273-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

Ä

Gaps

4

Length 318; Indels

```
7;
                                              ö
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Alnemri, Faresa
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: OF MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz 6 No. 6037461ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 318;
  4; Length 159;
                                           23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                               54 FXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                              5; Mismatches
    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
    14.5%; Score 40; 24.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%; Score 40; 33.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/859,167
                                                                                                                                                                                                                               Sequence 4, Application US/08859167
Patent No. 6037461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08859167
Patent No. 6037461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible OPERATING SYSTEM: WINDOWS SOFTWARE: WordPerfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(FILNG DATE:
CLASSTORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 33.3.
Transfer Conservative
                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-859-167-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Phile STATE: PA COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                        RESULT 4
US-08-859-167-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-859-167-6
                                                                                       õ
                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3751, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:
TITLE OF INVENTION:
ELLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR PAPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-01-08
PRIOR FILING DATE: 1997-01-08
PRIOR FILING DATE: 1997-01-08
FILING APPLICATION NUMBER: US 60/055,779
RIOR APPLICATION NUMBER: US 60/055,779
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                           ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,639
          Sequence 4, Application US/09517639
Patent No. 6414120
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo M.
TITLE OF INVENTION: Mammalian Deep Orange Proteins
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/904,452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1240.004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Potter, Jane E.R.
REGIESTRATION NUMBER: 33.33
REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (510) 923-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 31-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (510) 655-3542 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             973 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 QGXRXFXXWKGSVVDSV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-517-639-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-001C-3751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Staph
US-09-134-001C-3751
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
US-09-517-639-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
```

q ò

```
US-08-904-452-4
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3751, Ap
4, Appli
6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2, Appli
4909, Ap
3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2, Appli
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
                                                                                                                                                             8, 2002, 19:24:15; Search time 5.14706 Seconds (without alignments) 514.481 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6 Sequence 4 Sequence 4 Sequence 5 Sequence 5 Sequence 5 Sequence 5 Sequence 7 Sequence 7 Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 3 Sequence 4 Sequence 4 Sequence 4 Sequence 5 Sequence 5 Sequence 6 Sequence 6 Sequence 7 Sequence 7 Sequence 7 Sequence 7 Sequence 7 Sequence 6 Sequence 6 Sequence 7 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                          US-09-840-743-71
275
1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-904-452-4
US-09-517-639-4
US-09-134-001C-3751
US-08-859-167-4
US-09-109-273-4
US-09-273-4
US-09-273-6
US-09-273-6
US-09-273-6
US-09-273-6
US-09-273-6
US-09-273-6
US-09-273-7
US-09-627-412C-317
US-08-602-359A-33
US-09-641-256-2
US-09-199-637A-405
US-09-199-637A-405
US-09-199-637A-405
US-09-193-134-001C-4909
US-08-326-119A-13
US-08-937-195-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-858-207A-363
US-08-715-204-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US96-07627-3
US-08-471-119A-2
                                                                                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318
318
318
318
318
318
491
646
646
647
647
1198
1198
1198
11127
11127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                     November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.5
                                                                                                                     OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                    Sednence:
                                                                                                                                                                     uo
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
```

```
6
Sequence 2, Appli
Sequence 39, Appl
Sequence 39, Appl
Sequence 31, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appl
Sequence 11, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orange Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 31-JUL-1997
CLASSIFICATION: 435
US-08-937-102-2
US-09-070A-39
US-09-315-179-39
US-09-315-179-39
US-09-52-656-38
US-09-324-867-5
US-08-670-707A-37
US-09-315-179-37
US-09-315-179-37
US-09-315-179-37
US-09-131-179-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1240.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2718
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Randazzo, Filippo M.
TITLE OF INVENTION: Mammalian Deep (NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/08904452; Patent No. 6083742; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 973 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 QGXRXFXXWKGSVVDSV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4560 Horton St.
CITY: Emeryulle
STATE: California
COUNTR: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                  1443
1467
22115
22133
22133
22133
3898
3898
365
365
108
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-904-452-4
```

THIS PAGE BLANK (USPTO)

سر ن

```
Search completed: November 8, 2002, 19:29:40 Job time : 4.79412 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Meyers,
SOFTWARE: Fast
SEQ ID NO 2
LENGTH: 666
                                                                                                                                                                                                                                                                                                                                                                           US-09-799-875-2
                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                         APPLICANT: FLECKENSTEIN, Bernhard
APPLICANT: FLECKENSTEIN, BERNAPHORIN L (H-SEMAL) AND
TITLE OF INVENTION: HUMAN SEMAPHORIN L (H-SEMAL) AND
CORRESPONDING SEMAPHORINS IN OTHER SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%; Score 38; DB 10; Length 666; 58.3%; Pred. No. 53; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Frommer Lawrence & Haug LLP
STREET: 745 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lawrence, William F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 514429-3647
TELECOMMUNICATION INFORMATION:
TELEPRONE: 212-588-0800
TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09764587A
Fatent No. US20020106722A1
GENERAL INFORMATION:
APPLICANT: David Michalovich
APPLICANT: Philip David Hayes
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFRENCE: GP-30039-D1
CURRENT APPLICATION NUMBER: US/09/764,587A
CURRENT FILING DATE: 2001-01-18
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/836,077
FILING DATE: 16-Apr-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: amino acid
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-836-077-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 666 amino acids
                                                                                                                                                     Sequence 3, Application US/09836077 Patent No. US20020037851A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                      |:| | | | | : : 86 GIFTTPNFDETSSATTISTS 105
67 GVFLTQNXDXXSSXAXMXXA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: n/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 GXRXFXXWKGSV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 GPRIFAVWKGHV 62
                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-764-587A-2
                                                                                                                              US-09-836-077-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
ò
                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. US20020034780Alel Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: 35800/20996
CURRENT APPLICATION NUMBER: US/09/799,875
CURRENT APPLICATION NUMBER: 05/182,059
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Fast5EQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                               Gaps
                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                          Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 38; DB 10; Length 879; 30.3%; Pred. No. 72;
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Indels
                                                                                                                                                                                           5,
                                                                                                                                                        DB 10;
53;
                                                                                                                                                      Score 38; DB 1
Pred. No. 53;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 KNSKRDYLSSSFLCSDDDRASKNISMNSDSSFP 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 KGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/09799875 ; Patent No. US20020034780A1
                                                                                                                                                      13.8%;
ilarity 58.3%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.85
Best Local Similarity 30.37
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Meyers, Rachel
                                                                                               ; ORGANISM: HOMO SAPIENS
US-09-764-587A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-799-875-2
                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                      | | | | || |
51 GPRIFAVWKGHV 62
                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                              50 GXRXFXXWKGSV
```

```
Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PT223
CURRENT FILLING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xaa equals any of the naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 10; Length 21
Pred. No. 14;
5; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FeatSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 GPAIFIGWAGSALVILGGALLSCSCPGNESKAGYRAPRSYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 GXRXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 38; DB 10;
35.0%; Pred. No. 37;
tive 3; Mismatches 10
                                                                                              APPLICATION NUMBER: US/09/935,390A FILING DATE: 22-Aug-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                        NAME: Jane E. R. Potter
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: No. US20020076761Ale SEQUENCE DESCRIPTION: SEQ ID NO: 36.05-09-935-390A-36
                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,671
FILING DATE: 1997-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1235, Application US/09764864 Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                           TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 210 amino acids
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
  MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%;
24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 35.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (494)
; OTHER INFORMATION:
US-09-764-864-1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (14)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (488)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (493)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-764-864-1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                          .;
0
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                          ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 184;
                                                                                                  DB 10; Length 646;
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia, Pablo
Milliams, Lewis T.
Kothakota, Srinivas
TITLE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 10;
Pred. No. 12;
3; Mismatches 6
                                                                                                                                                                                                       326 RTLAFINNMSGDCGGAISADTQISITDTVKGILFENN 362
                                                                                                                                                                              37 RXXXFIXRMXXXQGXRXFXXWKGSVVDSVXGVFLTQN 73
                                                                                                                       Pred. No. 34;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: DIVERII80-2
CURRENT APPLICATION NUMBER: US/09/903,410
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/382,242
PRIOR APPLICATION NUMBER: US 08/602,359
PRIOR PRICATION NUMBER: US 08/602,359
PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
                                                                                                Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/09935390A Patent No. US20020076761A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/09903410 Patent No. US20020146799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Staphylothermus Marinus US-09-903-410-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 GXRXFXXW---KGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-841-132-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Escobedo, Jaime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.8%;
Best Local Similarity 45.8%;
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DIVERSA CORPORATION
                                                                                                Query Match
Best Local Similarity 27.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quianjin, Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINK, Steven
SWANSON, Ronald
WARREN, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Emeryville STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAFFIA, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    ROBERTSON, Dan
MURPHY, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                           REID, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-935-390A-36
                                                                                                                                                                                                                                                                                               US-09-903-410-33
LENGTH: 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                              ò
```

ö

g

```
APPLICANT: CALIMER, Alan
APPLICANT: Alfano, James R.
APPLICANT: Alfano, James R.
APPLICANT: Alfano, James R.
APPLICANT: Charkowski, Amy O.
TITLE OF INVENTION: HRP PATHOGEULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
TITLE OF INVENTION: HRP PATHOGEULITY ISLAND AND THEIR USES
FILE REFERENCE: 19603/3243
CURRENT APPLICATION NUMBER: 05/09/825,414
CURRENT FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 91
SOFTWARR: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Brasiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND FILE REFERENCE: 210.121.49Cg
CURRENT APPLICATION NUMBER: US/09/841,132
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                             DB 10; Length 305;
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.2%; Score 39; DB 10; Length 316; 53.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudomonas syringae pv. delphinii
US-09-825-414-56
                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                Score 39;
Pred. No.
PRIOR APPLICATION NUMBER: 60/178,227
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/220,590
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEO ID NOS: 95
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 317, Application US/09841132 Patent No. US20020061848A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-825-414-56
; Sequence 56, Application US/09825414
; Patent No. US20020083489A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                14.2%;
38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                           | | | : |: |||
146 FALWLGGTIHSLVQTFLT 163
                                                                                                                                                                                                                                                                                                                                                                                             54 FXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 KGQLIDLVSGAFL 113
                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-761-288-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 KGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-09-841-132-317
                                                                                                                                                                         LENGTH: 305
                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORMATION:

APPLICANT: Padigaru, Muralidhara
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Taupier, Raymond J
APPLICANT: Tolenew, Velizar
APPLICANT: Tolenew, Velizar
APPLICANT: Tolenew, Velizar
APPLICANT: Li, Li
TITLE OF INVENTION: No. US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam
FILE REFRENCE: 15966-638
CURRENT APPLICATION NUMBER: 05/09/761,288
CURRENT APPLICATION NUMBER: 60/177,839
PRIOR APPLICATION NUMBER: 60/175,349
PRIOR APPLICATION NUMBER: 60/175,349
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/220,253
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR PRIOR PRIOR PRIOR NUMBER: 60/220,253
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
                                                                                                                                                                                                                                                                                                                              APPLICANT: COllmer, Alan
APPLICANT: Collmer, Alan
APPLICANT: Collmer, Alan
APPLICANT: Collmer, James R.
APPLICANT: Charkowski, Amy O.
APPLICANT: Charkowski, Amy O.
ATILE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
CURRENT APPLICATION NUMBER: 05/09/825,414
CURRENT APPLICATION NUMBER: 60/224,604
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,648
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 22
LENGTH: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                  3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
     Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 241;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
14.4%; Score 39.5; DB 10; all arity 37.0%; Pred. No. 5.7; Conservative 4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 10;
Pred. No. 11;
2; Mismatches 4,
                                                                                                                           126 KGEVADLTISLAGKIISQNLDSHAHKA 152
                                                                                             58 KGSVVD---SVXGVFLTQNXDXXSSXA 81
                                                                                                                                                                                                                                                                 Sequence 22, Application US/09825414 Patent No. US20020083489A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 86, Application US/09761288 Patent No. US20020065405A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-09-825-414-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.2
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 KGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . || ::| | | ||
66 KGQLIDLVSGAFL 78
Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                             US-09-825-414-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-09_761-288-86
```

δ qq

```
3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yandamoto, Robert T.

APPLICANT: Xu, Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: PROMATYCES

TITLE OF INVENTION: PROMATYCES

CURRENT ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/2191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39.5; DB 10;
Pred. No. 5.7;
       CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/245,578

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-2

PRIOR FILING DATE: 2000-12-2

PRIOR FILING DATE: 2001-12-2

PRIOR FILING DATE: 2001-12-2

PRIOR FILING DATE: 2001-12-3

PRIOR FILING DATE: 2001-12-3

PRIOR FILING DATE: 2001-12-3

PRIOR FILING DATE: 2001-12-3

PRIOR FILING DATE: 2001-12-16

NUMBER OF SED ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
  CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13630, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 KGEVADLTISLAGKIISQNLDSHAHKA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 KGSVVD---SVXGVFLTQNXDXXSSXA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.48;
37.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-815-242-13630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-815-242-13630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
                 FILE REFERENCE: 4121-120
CURRENT APPLICATION WUMBER: US/09/733,167
CURRENT FILING DATE: 2006-12-08
PRIOR APPLICATION NUMBER: PCT/DE99/01712
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1998-06-08
PRIOR FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 8
SOFFWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/733,167
CURRENT APPLICATION NUMBER: 2000-12-08
CURRENT FILING DATE: 2000-12-08
PRIOR PILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
PRIOR FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 10; Length 318;
Pred. No. 9.9;
8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09733167
Patent No. US20020099009A1
GENERAL INFORMATION:
APPLICANT: Feter, Marcus
APPLICANT: Krammer, Peter
TITLE OF INVENTION: Protein for Regulation of Apoptosis
FILE REFERENCE: 4121-120
TITLE OF INVENTION: Protein for Regulation of Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5%; Score 40; 33.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13509, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 WRDYINGSLLEALKGVFITDS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 WRDYINGSLLEALKGVFITDS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.3%;
Matches 7; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Mus musculus
US-09-733-167-3
                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-733-167-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-815-242-13509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318
                                                                                                                                                                                                                                                                  LENGTH: 318
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-733-167-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

.; H

Gaps

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

8, 2002, 19:26:04; Search time 2.79412 Seconds . November Run on:

(without alignments)
464.428 Million cell updates/sec

Title: Perfect score:

US-09-840-743-71
275
1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

92612 Total number of hits satisfying chosen parameters:

92612 segs, 14418503 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

/cgn2_6/ptodata/1/pubpaa/usus_....._.pep:*/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/USI0_NEW_PUB.pep:*/cqn2_6/ptodata/1/pubpaa/USI0_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 6, Appli	Sequence 1, Appli	3	135	Sequence 13630, A	Sequence 22, Appl	Sequence 86, Appl.	Sequence 56, Appl	Sequence 317, App	Sequence 33, Appl	Sequence 36, Appl	_	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	73		Sequence 26, Appl	
QI	US-09-733-167-6	US-09-733-167-1	US-09-733-167-3	US-09-815-242-13509	US-09-815-242-13630	US-09-825-414-22	US-09-761-288-86	US-09-825-414-56	US-09-841-132-317	US-09-903-410-33	US-09-935-390A-36	US-09-764-864-1235	US-09-836-077-3	US-09-764-587A-2	US-09-799-875-2	US-09-815-242-13543	US-09-995-587A-11	US-09-799-777-26	US-09-815-242-11729
DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Query Match Length DB	210	318	318	164	164	241	305	316	646	184	210	464	999	999	879	167	792	217	276
Query	14.5	14.5	14.5	14.4	14.4	14.2	14.2	14.2	14.2	13.8	13.8	13.8	13.8	13.8	13.8	13.6	13.6	13.5	13.5
Score	40	40	40	39.5	39.5	39	39	39	39	38	38	38	38	38	38	37.5	37.5	37	37
Result No.	1	~	<u>ლ</u>	4	വ	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 37331, A sequence 6, Appli Sequence 42016, A Sequence 11074, A Sequence 1153, App Sequence 216, App Sequence 21	Sequence 41743, A Sequence 270, App Sequence 22, Appl Sequence 1, Appli Sequence 1, Appli Sequence 4958, Ap
US-09-864-761-3 US-10-052-586-6 US-09-864-761-4 US-09-815-242-1 US-09-815-242-1 US-09-927-58-21 US-09-987-722-2 US-09-989-723-2 US-09-989-731-2 US-09-989-731-2 US-09-989-731-2 US-09-989-731-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2 US-09-991-163-2	US-09-864-761-41743 US-09-939-980-270 US-09-911-8654-22 US-09-816-248-1 US-09-815-242-4958
4U	59 90 99 118 307
29.00.00.00.00.00.00.00.00.00.00.00.00.00	12.7 12.7 12.7 12.7 12.7
01222222222222222222222222222222222222	444 444 544

## ALIGNMENTS

```
US-09-733-167-6

US-09-733-167-6

Sequence 6, Application US/09733167

Patent No. US20020099009A1

GENERAL INFORMATION:

APPLICANT: Peter, Marcus

APPLICANT: Peter, Marcus

TITLE OF INVENTION: Protein for Regulation of Apoptosis

TITLE OF INVENTION: Protein for Regulation of Apoptosis

TITLE OF INVENTION: Protein for Regulation of Apoptosis

CURRENT PELING DATE: 2000-12-08

PRIOR PELING DATE: 1999-06-08

PRIOR FILING DATE: 1999-06-08

PRIOR FILING DATE: 1999-06-08

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Version 3.1

FEATURE OF SECTION OF THE PATENCY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: C-DEDD, which is a deletion mutant of human DEDD comprising am; OTHER INFORMATION: acids 109-318 of the naturally occurring humna DEDD. US-09-733-167-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
```

Gaps 4 Query Match 14.5%; Score 40; DB 10; Length 210; Best Local Similarity 33.3%; Pred. No. 6.2; Matches 7; Conservative 8; Mismatches 2; Indels

;

|: |::::::|||:::::152 WRDYINGSLLEALKGVFITDS 172 57 WK----GSVVDSVXGVFLTQN 73 δλ Dp

RESULT 2

US-09-733-167-1
Sequence 1, Application US/09733167
Patent No. US20020099009A1
GENERAL INFORMATION:
APPLICANT: Peter, Marcus
APPLICANT: Krammer, Peter

œ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         Leo C.P., Hsu S.Y., McGee E.A., Salanova M., Hsueh A.J.W.; "DEFT, a novel death effector domain-containing molecule predominantly expressed in testicular germ cells."; Endocrinology 139:4839-4848(1998).
                               Stegh A.H., Schickling O., Ehret A., Scaffidi C., Peterhaensel C., Hofmann T.G., Grummt I., Krammer P.H., Peter M.E.; "DEDD, a novel death effector domain-containing protein, targeted to the nucleolus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I- SUBUNT: Interacts with caspase-8 and FADD (By similarity).
-I- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus during CD95-mediated apoptosis where it is localized in the nucleoli (By similarity).
-I- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.
-I- SISUE SPECIFICITY: Widely expressed with highest levels in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: Binds strongly and non-specifically to DNA. Induces apoptosis. Inhibits DNA transcription in vitro (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50168; DED; 1.
Apoptosis; Transcription regulation; Repressor; DNA-binding; Nuclear protein; Alternative splicing.
DOMAIN 25 103 DED.
                                                                                                                                                                                                                                                                                                                               Pan G.;
"FLDED-1, a novel molecule with a DED-like domain.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   Thome M., Tschopp J.; "DEDPRO1, a novel DED-containing protein."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao Z., Huang X., Li N., Zhu X., Cao X.;
"A novel gene from human dendritic cell.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             testis.
-!- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY TISSUE-Testis; MEDLINE-99049260; PubMed-9832420;
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-98447599; PubMed=9774341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Bone marrow, and Placenta;
Strausberg R.;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [5]
SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF083236; AAC33105.1; -. EMBL; AF100341; AAD16414.1; -. EMBL; AF043733; AAC80280.1; -. EMBL; AJ010973; CAA09445.1; -. EMBL; AF064605; AAC17110.3; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC016724; AAH16724.1;
EMBL; BC013910; AAH13910.1;
Genew; HGNC:2755; DEDD.
                                                                                                             EMBO J. 17:5974-5986(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001875; DED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01335; DED; 1.
SMART; SM00031; DED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:2755; DEDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
                                                                                              the nucleolus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 606841;
                                                                                                                                                                                                                                                                                                                           Pan G.
```

```
ä
D -> GEBIQGFQRWSRLEGEYKELLGHWAVYAIQY (IN ISOFORM 2).
                                                                                                  Gaps
                                                                                                    4
                                                                   Ouery Match 14.5%; Score 40; DB 1; Length 318; Best Local Similarity 33.3%; Pred. No. 24; Matches 7; Conservative 8; Mismatches 2; Indels
                           P -> L (IN REF. 5).
FF9D5FF9B61F6BB6 CRC64;
                                                                                                                                                                                                  8, 2002, 19:27:09
                                                                                                                                                          260 WRDYINGSLLEALKGVFITDS 280
                                            36794 MW;
                                                                                                                              57 WK----GSVVDSVXGVFLTQN 73
  194
                                                                                                                                                                                                     Search completed: November
                           13
318 AA;
                                                                                                                                                                                                                 Job time : 5.23529 secs
  194
  VARSPLIC
                                             SEQUENCE
                              CONFLICT
     FFFS
                                                                                                                                                            q
                                                                                                                                   ò
```

Dp

à

```
211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, BC008104; AAH08104.1; -...
MGD: MGI:1859285; Cldn7.
InterPro; IPR004031; PMP22_Claudin.
InterPro; PR004031; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1...
PROSITE; PR01346; CLAUDIN.
Tight junction; Transmembrane.
     PRT;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-99110921; PubMed-9892664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF087825; AAD09760.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22359 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102
                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
  CLD7_MOUSE
Q9Z261;
                                                                                                                                         Claudin-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEDD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
        HID DAY NEW KRANK REPORTED THE COLOR OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                              Score 41; DB 1; Length 1391;
Pred. No. 78;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%; Score 40; DB 1; Length 191; 24.4%; Pred. No. 14;
                                 HSSP; Q9KWU7; 1HQM.
InterPro; IPR001572; RNA_pol_B.
Pfam; PF00562; RNA_pol_B. 1.
Transferase; Transcription; DNA-directed RNA polymerase; Complete proteome.
SEQUENCE 1391 AA: 15557 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keen T.J., Inglehearn C.F.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
--- SUBCELLILAR LOCATION: Integral membrane protein.
--- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83B445908DFFF41A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 GXRXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001832; Claudin.
InterPro; IPR004031; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
PRINTS; PR01077; CLAUDIN; 1.
PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ011811; CAA09790.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20366 MW;
                                                                                                                                                                                                                                                                                              14.9%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.48;
                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 64.5.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 KNSATSSVDGVFLT 131
                                                                                                                                                                                                                                                                                                                                                                                                         58 KGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claudin-7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
100
141
191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
tes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLD7_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morita K., Furuse M., Fujimoto K., Tsukita S.; "Laudin multigene family encoding four-transmembrane domain protein components of tight junction strands "; Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEDD_HUMAN STANDARD, PRT; 318 AA.

075618, 060737;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation)
16-JUN-2002 (Rel. 41, Created)
16-JUN-2002 (Rel. 41, Last annotation)
16-JUN-2002 (Rel. 41, Created)
16-JUN-2002 (Rel. 41, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. 4FE87F3A57AC9F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 GPAIFIGWAGSALVLLGGALLSCSCPGSESKAAYRAPRSYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 GXRXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%; Score 40; DB 1; 24.4%; Pred. No. 16;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NX OCC BEE DE STAN
```

ö

TRANSMEM

SEQUENCE Query Match

Matches

RESULT 14 CLD7_MOUSE

g ŏ

```
Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {RNA}(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPOB_MYCPN
ID RPOB_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P78013;
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peterson M.D., Novak K.D., Reedy M.C., Ruman J.I., Titus M.A.;
"Molecular genetic analysis of myoc, a Dictyostelium myosin I.";
J. Cell Sci. 108:1093-1103(1995).
-!- FUNCTION: MYOSIN IS A PROPEIN THAT BINDS TO ACTIN & HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY ACTIN.
-!- SUBUNIT: MYOSIN I HEAVY CHAIN IS SINCLE-HEADED. DIMER OF A HEAV
AND A LIGHT CHAIN. INABILITY TO SELF-ASSEMBLE INTO FILAMENTS.
-!- SIMILARITY: CONPAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 1; Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; CBS domain; Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E3A0F57ABE8FB323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyostellium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-AX2;
MEDLINE-95348228; PubMed-7622596;
                                                                                                                                                                                                                                                                                                                                                             EMBL; Y14082; CAA74500.1; -. EMBL; Z99109; CAB12794.1; -. Subtilist; BG13022; yhdp. InterPro; IPR000644; CBS_domain. InterPro; IPR005170; CorC_HlyC. InterPro; IPR002550; DUF21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00571; CBS; 2.
Pfam; PF01595; DUF21; 1.
Pfam; PF03471; CorC_H1yC; 1.
SMART; SM00116; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 VDTIGGWFLTQKYD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 VDSVXGVFLTQNXD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myosin IC heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
TRANSMEM 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYOC OR DMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYSC DICDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
RRARE REPAIR OF THE REPAIR OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 24:4420-4449(1996).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBSTRATES.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.9%; Score 41; DB 1; Length 1181; 31.6%; Pred. No. 66; 1. Indels of Mismatches 9; Indels of the state of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50002; SH3; 1.
Myosin; Actin-binding; ATP-binding; Chemotaxis; SH3 domain;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132915 MW; 5EB1EE47F0CA8803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON ALPHA-HELICAL, ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1391 AA.
                                                                                                                                                                                                                                                                                                                         Dictybb; DD01090; myoc.
InterPro; IPR001452; SH3.
InterPro; IPR001469; myosin_head.
Pfan; PF00018; SH3; 1.
Pfam; PF00063; myosin_head; 2.
PRINTS; PR00193; MYOSINIEAVY.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
PRODOM; PD0000355; myosin_head; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
                                                                                                                                                                                                                    EMBL; L35323; AAC37427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       653 WKGDALSACRAILASQNVD 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 WKGSVVDSVXGVFLTQNXD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \begin{array}{c} 1181 \\ 116 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1122 118
1181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                           1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
```

S

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y., Sato T., Scanlan E., Schlacher R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorkin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Waitzenegger T., Winters P., Wipat A., Yamane K., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: SPECIFICALLY METHYLATES THE GUANOSINE IN POSITION 1207 OF 16S RENA IN THE 30S PARTICLE (BY SIMILARITY).

CATALYTIC ACTIVITY: S-adenosyl-L-methionine + IRNA = S-adenosyl-L-homocysteine + IRNA containing N(2)-methylguanine.
                                                                                                                                                                                                                                      "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A POTENTIAL FRAMESHIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
81bosomal RNA small subunit methyltransferase C (EC 2.1.1.52) (rRNA (quanine-N(2)-)-methyltransferase) (165 rRNA m2G1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY. RSMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=TOKYO 1998;
MEDLINE-20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Score 41; DB 1; Length 260; 41.7%; Pred. No. 13; Live 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 protein; Complete proteome.
260 AA; 28258 MW; 363B6DDF017BE77E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                   !- SIMILARITY: BELONGS TO THE UPF0028 (SWS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 KGSVSDAVRASISIPGIFIPQRLD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGSVVD-----SVXGVFLTQNXD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Subtilist, BG13363; ylbk.
InterPro; IPR002641; Patatin.
InterPro; IPR001423; UPF0028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01734; Patatin; 1.
PROSITE; PS01237; UPF0028; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z98682; CAB11357.1; -. EMBL; Z99111; CAB13377.1; -.
                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSMC OR BU328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSMC_BUCAI
P57413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
        δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseefisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              **X MEDLINE-94044033; PubMed-93483//;

**A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

**A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

**A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

**A Azevedo V., Bertero M.G., Brans A., Brun M., Brignell S.C., Bron S.,

**Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

**A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

**A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

**A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

**A Britz C., Fujita M., Fujita Y., Fumas S., Galiszi A., Galleron N.,

**A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

**A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

**A Hilbert H., Holsappel S., Haga K., Halech J., Harwood C.R., Hendut A.,

**A Hilbert H., Holsappel S., Haga K., Halech J., Lazarevic V.,

**A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

**A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

**A Kurita K., Levine A., Liu H., Misuda S., Manel C., Medigue C.,

**A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

**A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

**RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

**A Reger M., Rivolta C., Rocha E., Roche B., Ros M., Sadale Y.,

**A Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

**A Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

**RA Reger M., Tackonla B., Takagi T., Taraka T., Tarkagiar T.,

**A Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

**A Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

**A Tosato V., Wannier E., Wedler E., Wedler T.,

**A Tosato V., Ordiva M. Wedler E., Wedler F.,

**A Tosato V., Ordiva M. Wedler E., Wedler F.,

**A Tosato V., Ordiva M. Wedler E., Wedler F.,

**A Tosato V., Ordiva M. Wedler E., Wedler F.,

**A Tosato V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP001119; BAB13036.1; ALT_FRAME.
InterPro; IPR002052; N6_Mtase.
InterPro; IPR000051; SAM_bind.
PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
FRNA Processing; Transferase; Methyltransferase; Complete proteome.
SEQUENCE 338 AA; 39105 MW; E43516DDD22FA014 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 1;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  007585;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
WAS CORRECTED IN POSITION 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | : |: || : | | WKNLIIKSLPGVFGHKKIDSGS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 WKGSVVDSVXGVFLTQNXDXXS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 30.v.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YHDP_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YHDP_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCOOS SON SERVING SER
```

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                               YLBK_BACSU
034731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                              Query Match
                                                               region
                                                                                                                                                                                                                                                                                                                                                                                                                                      YLBK_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                      g
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Benes V., Arnold L., Smrt J., Paces V.; "Nucleotide sequence of the right early region of Bacillus phage phi 15 and comparison with related phages: reorganization of gene 17 during evolution."; Gene 75:341-347(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Phage PZA;
MEDLIAE-87031575; PubMed-3095189;
Paces V. Vlock C. Urbanek P., Hostomsky Z.;
"Nucleotide sequence of the right early region of Bacillus subtilis phage PZA completes the 19366-bp sequence of PZA genome. Comparison with the homologous sequence of phage phi 29.";
Gene 44:115-120(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
-i- INDUCTION: Highest expression in darkness.
                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                        Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                 6D9CFC6C2C2395BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 1;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Early protein GP16.9.
                                                                                                                                                                                                            Transport; Transmembrane; Multigene family. TRANSMEM 15 37 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA
                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                           EMBL; AF118858; AAG11397.1; -.
InterPro; IPR001905; Ammonium_transp.
Pfam; PP00909; Ammonium_transp: 1.
TIGRPAMS; TIGR00836; amt; 1.
PROSITE; PS01219; AMMONIUM_TRANSP; 1.
                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=Phage phi-15;
MEDLINE=89232766; PubMed=2497055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA sphi-29-like viruses.
NCBI_TaxID=10757, 10755, 10756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                  49652 MW;
                                                                                                                                                                                                                                                                                                                                                                        15.3%;
                                                                                                                                                                                                                                                                                                                                                                                   42.98;
                        TRANSPORTERS (TC 2.49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage PZA,
Bacteriophage phi-15, and
Bacteriophage phi-29.
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        57 WKGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                       5 WEASVTDSINAIYL 18
                                                                                                                                                                                                                                                                                                                                               460 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VG69_BPPZA
P08388;
                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                         TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunst F., Journal, J. F., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., A Borriss R., Burachi C.V., Caldwell B., Capuano V., Carter N.M., Broullet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Benian K.D., Errington J., Fabrer C., Ferrari E., Foulger D., Ramerson P.T., Frizz C., Fujita M., Fujita Y., Fuma S., Calizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Ghim S.Y., Glaser P., Koffeau A., Golightly E.J., Grandi G., Albert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C., Akobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Aurita K., Layldus A., Liu H., Masuda S., Mauel C., Medigue C., Median N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
SPECIES-Phage phi-29;
MEDLINE-66165872; PubMed-3007295;
Garvey K.J., Yoshikawa H., Ito J.;
"The complete sequence of the Bacillus phage phi 29 right early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bertero M., Presecan E., Glaser P., Richou A., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.9%; Score 41; DB 1; Length 108; 35.0%; Pred. No. 5.3; ive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Bacillus subtilis chromosomal region downstream nprE."; Submitted (AUG-1997) to the {\tt EMBL/GenBank/DDBJ} databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 AA; 12648 MW; 4FA9C051B60CD8F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein ylbK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M1813; AAA88498.1; --
EMBL; M28830; AAA32330.1; --
EMBL; M14430; AAA88350.1; --
PIR; E29004; WRBP69.
PIR; JS0193; WRBP13.
PIR; JN0031; JN0031.
Early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 RXFXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 RRFASWSGQLLEGSNSVFWT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 35.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                             Gene 40:301-309(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1423;
```

```
Spindlin homolog (Protein DXF34).
DXF34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AT13_LYCES
Q9FVNO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                               Heath P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AT13_LYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/2r send an email to license@ib-sib.ch).
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: Tricarboxylic acid cycle.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINCE; FROUGES; CITALAGESTICALS.
PROSITE; PSOUGHOS, CITRATE_SYNTHASE; 1.
Lyase; Tricarboxylc acid cycle; Mitochondrion; Transit peptide.
TRANSIT 1 7 MITOCHONDRION (BY SIMILARITY).
CHAIN 7 475 CITRATE SYNTHASE.
ACT_SITE 310 BY SIMILARITY.
ACT_SITE 356 356 BY SIMILARITY.
ACT_SITE 411 411 BY SIMILARITY.
SEQUENCE 475 AA; 52153 MW; F93525B3F31FCB3F CRC64;
                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oshida Y., Miyake K., Kanayama S., Kirimura K., Usami S.,
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Citrate + COA = acetyl-COA + H(2)0
                     DB 1; Length 474;
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 1; Length 475; Pred. No. 12;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                 01-00T-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citrate synthase, mitochondrial precursor (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAPABLE OF OXIDATIVE METABOLISM. SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPIH_HUMAN STANDARD; PRT; 232 AA. 099865, 075650; Q9UJU0; DI-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                     Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002020; Citrate_synt.
                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; Processor Citrate_S
Processor Citrate_Synt; 1
PRINTS; PRO0143; CITRTGNTHASE.
PROSITE; PS00480: CITRPATE CVNT
                     15.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D63376; BAA09691.1; -. HSSP; P23007; 2CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.6%;
58.3%;
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                 |:|||:|| |:
89 WEGSVLDSEEGI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|||:|| |:
89 WEGSVLDSEEGI 100
Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                       57 WKGSVVDSVXGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 WKGSVVDSVXGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oxaloacetate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-WU-2223L;
                                                                                                                                                                                                                                                   CISY_ASPNG
P51044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
SPIH_HUMAN
ID SPIH_HU
AC 099865,
DT 01-NOV-
DT 16-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                a
                                                                                                                                                                                                                                                            HDD BRAND BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               von Wiren N., Lauter F. R., Ninnemann O., Gillissen B., Walch-Liu-P., Engels C., Jost W., Frommer W.B.; "Differential regulation of three functional ammonium transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes by nitrogen in root hairs and by light in leaves of tomato."; Plant J. 21:167-175(2000).
-i- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-i- TISSUE SPECIFICITY: Leaves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Asteridae, euasterids I; Solanales; Solanaceae; Solanum.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                     MEDLINE-97419273; PubMed-9271673;
Laval S.H., Reed V., Blair H.J., Boyd Y.;
"The Structure of DXF34, a human X-linked sequence family with
homology to a transcribed mouse Y-linked repeat.";
Mamm. Genome 8:689-691(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C -> R (IN REF. 2).
T -> A (IN REF. 2; CAA18149).
093E7E9F5340BF71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.3%; Score 42; DB 1; Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. 
-1- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation; Cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ammonium transporter 1, member 3 (LeAMTI;3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 8.1; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20208060; Pubmed-10743657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AL022157; CAA18148.1; -. EMBL, A4022157; CAA18149.1; -. InterPro; IPR003671; Spin.Ssty. Pfam; PF02513; Spin.Ssty; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26536 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y09858; CAA70988.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGDEPITOWKGTVLDQV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 protein;
196 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGXRXFXXWKGSVVDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 AA;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4081;
```

```
P23007;
                                                                                                                                                                                                                                                                                                       CISY_EMENI
000098;
                                                                                                 ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                           CISY_EMENI
                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                  õ
                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ueda M., Sanuki S., Kawachi H., Shimizu K., Atomi H., Tanaka A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Citrate + CoA = acetyl-CoA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Tricarboxylic acid cycle.
-!- SUBCELLULAR LOCATION: Mitchondrial matrix.
-!- MISCELLANEOUS: CITRARE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida tropicalis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
           SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE UPP0053 FAMILY. SIMILARITY: CONTAINS 2 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 1; Length 442; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                               Pfam; PF03471; CorC_HlyC; 1.
Hypothetical protein; CBS domain; Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citrate synthase, mitochondrial precursor (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                             POTENTIAL.
E2EA41573549DA83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467 AA
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                    Subtilist; BG11695; YqhB.
InterPro; IPR000644; CBS_domain.
InterPro; IPR005510; CorC_HlyC.
InterPro; IPR002550; DUF21.
Pfam; PF00551; CBS; 2.
Pfam; PF01595; DUF21; 1.
                                                                                                                                                                                                                                                                                                                                          MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB001565; BAA19410.1; -.
                                                                                                                                                                                                                                                                                                                                                                 17.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            396 VDTLGGWFLTQNIDAEPESA 415
                                                                                                                                                              EMBL; D84432; BAA12531.1; -. EMBL; Z99116; CAB14406.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                              130
49956 N
                                                                                                                                                                                                                                                                                                                                                                                                                    VDSVXGVFLTQNXDXXSSXA
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                          442 AA;
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oxaloacetate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-5482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-PK233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CISY_CANTR
P79024;
                                                                                                                                                                                                                                                                                                                             TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CISY_CANTR
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Tricarboxylic acid cycle.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- MISCELLANBOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CAPABLE OF OXIDATIVE METABOLISM.
-!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyase, Tricarboxylic acid cycle, Mitochondrion, Transit peptide.

TRANSIT 1 35 MITOCHONDRION (POTENTIAL).

CHAIN 36 474 CITRATE SYNTHASE.

ACT_SITE 310 310 BY SIMILARITY.

ACT_SITE 356 BY SIMILARITY.

ACT_SITE 411 411 BY SIMILARITY.
                                                                                                     Lyase; Tricarboxylic acid cycle; Mitochondrion; Transit peptide. TRANSIT 1 ? MITOCHONDRION (POTENTIAL). CHAIN ? 467 CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBL_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 1; Length 467;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citrate synthase, mitochondrial precursor (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E2E86892ACB5398B CRC64;
                                                                                                                                                                                                                                                          4B194132C4198CA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 AA.
                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emericella nidulans (Aspergillus nidulans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002020; Citrate_synt.
Pfam; PF00285; Citrate_synt; 1.
PRINYS; PR00143; CITRTSNTHASE
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
InterPro; IPR002020; Citrate_synt.
Pfam; PF00285; citrate_synt. 1.
PRINTS; PR00143; CITRTSNTHASE.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=FGSC 4;
MEDLINE=97306446; PubMed=9163747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ×
                                                                                                                                                                                                                                                          52004 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U89675; AAC49728.1; -.
                                                                                                                                                                                                                                                                                                          15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52223
                                                                                                                                                                                                                                                                                                       Query Match 15.6
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                          467
301
347
402
                                                                                                                                                                                                                                                                                                                                                                                                            57 WKGSVVDSVXGV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|||:| : |:
79 WEGSVLDPIEGI 90
                                                                                                                                                                             301
347
342
402
467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310
356
411
474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxaloacetate.
```

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

November 8, 2002, 19:24:14; Search time 3.23529 Seconds (without alignments) 1153.796 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-840-743-71 275 1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues

Searched:

112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P54505 bacillus su			asper		Q91VnU Iycopersico		buchnera	bacillus	P42522 dictyosteli				075618 homo sapien		Q9z2k0 rattus norv					an			arabi		mus m			90	3257	mycop	3336
SUMMARIES	YQHB_BACSU	CISY_CANTR	CISY_EMENI	CISY_ASPNG	SPIH_HUMAN	ATI3_LICES	YLBK BACSU	RSMC_BUCAI	YHDP_BACSU	MYSC_DICDI	RPOB_MYCPN	CLD7_RAT	CLD7_MOUSE	DEDD_HUMAN	DEDD_MOUSE	DEDD_RAT	CISY_NEUCR	YRS7_CAEEL	CHP1_SCHPO	MRP6_HUMAN	YY46_ANASP	AKA9_HUMAN	ATPF_STRPN	CI30_ARATH	SPIN_HUMAN	SPIN_MOUSE	COX3_SCHCO	YE53_AQUAE	EBAG_STRPL	YG2O_YEAST	DP3B_MYCPU	UT1_HUMAN
DB	:	<del></del> .	٠,	٠,	٦,	٦,	٠.	7	ч	Н	Н	Н	_	_	_	<del>, -</del> 1	<b>,</b>	<del></del> 4 -	-	<b>-</b>	-	<b>-</b>	н,		-	Н	H	Н	-	Н	Н,	-
Length	1 47	9	474	4/5	737	108	260	338	444	1181	1391	191	211	318	318	318	469	967	960	1503	1526	3911	164	208	237	240	268	270	313	314	373	382
% Query Match	٠.	9.0			υ. 	n o		6.4																								
	; ;;;	H,	-4 -			7 2	7	1,	7	17	17	1,	1,	5	7	7	14	Ξ,	1	7	14	7	14	74	7.7	7	14	14	14	14	14	14
Score	47	43	4 <b>-</b>	Α. υ	4.2	47	41	41	41	41	41	40	40	40	40	40	40	40	40	40	40	₹,	39.5	بر و د	39	39	36	39	36	39	33	λ V
Result No.		Cit i	m •	գ+ ւ	n u	0 1	, ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	572	26	27	28	29	30	31	32	<b>3.</b>

P54428 bacillus su P02675 homo sapien	Q44052 arthrobacte P35315 trypanosoma P38008 chlamydia t	P58107 homo sapien P42780 bacteroides	P36324 raspberry r 09x4w3 vibrio chol	Q58254 methanococc 095471 homo sapien	09yh92 brachydanio
YRKA_BACSU FIBB_HUMAN	IMD_ARTGO ATC_TRYBB PMPF CHLTR	EPPL_HUMAN BPRX_BACNO	POL2_RRVS RTXC_VIBCH	MCRV_METJA	CLDX_BRARE
П Н	<del></del>				-
434	641 1011 1034	5065	1107	200	215
14.2 14.2	14.2	14.2	14.0 13.8	13.8	13.8
39 39	თ თ თ ო ო ო	38.5	38.5	388	38
34 35	36 37 38	39	41	443	45

## ALIGNMENTS

THIS PAGE BLANK (USPTO)

6

```
flowering time; endosperm development; MEDEA.
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATRODOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a prometer at least 70% identical to DMTs, flanking sequence, DMT 3 flanking sequence or an 5 ' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein. The expression cassette is polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably adrobacterium by sexual cross, and selecting a host cell preferably in flowering time, introduction of the protein in a plant results in a delay in flowering time, introduction of the protein in a plant results in a delay in flowering time, introduction of the protein in an Arabidopsis leaf results in modulation of methylation of protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. The protein of target genes by demethylation. The present repulses and regulates as sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                       New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
                                                                                                                                                                                                                    Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 79; DB 23; Length 20
44.2%; Pred. No. 2.3e-08;
:ive 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 KXXXXLRTEHXVXXLPDXHXXLXX-----XDXXXYLLXIWXP 140
                                                                                                                                                                                                                    Okamuro JK,
                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 90; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU72750 standard; Protein; 108 AA
                                                                                                                                                                                                                    Hannon M,
                                                                                                                               23-APR-2001; 2001WO-US13059.
                                                                                                                                                          21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 44.2
Matches 19; Conservative
                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                  Choi Y,
                                                                                                                                                                                                                                             WPI; 2002-055307/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wheat DMT3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 AA;
                                                                                                                                                                                                                                                            N-PSDB; AAS96704
                                                                      WO200180626-A1
                                                                                                                                                                                                                 Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2002
                                           Glycine max
                                                                                                  01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU72750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU72750
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMPTER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5. flanking sequence, DMT 3. flanking sequence or an 5. untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a crossing a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into-a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of chromosomal DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in expression of the protein in an Arabidopsis leaf results in expression of the protein in an Arabidopsis leaf results in expression of the protein in an Arabidopsis leaf results in expression of the protein in an Arabidopsis leaf results in expression of the DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in expression of the protein in a DNA in the cell, reducting a nucleic acid in a sample. DEMETER is related to 5-methylotycine glycosylases and regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising a sequence or C -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 FADHKSSYDPIYVAREQLWKLERRMVYFGTSVPSIFKGLTTEEIQQCFWKGFVCVRGFER 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide that control plant development com
having a specific homology to DEMETER domains A,B or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.1%; Score 77; DB 23; Best Local Similarity 29.5%; Pred. No. 3.1e-08; Matches 23; Conservative 0; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8, 2002, 19:26:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a DMT-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 87; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hannon M,
                                                                                                                                                                                                                                             23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                          21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 XXXXPXXLXXXLHXXXSK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETGAPRPLCQHLHVAASK
                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: November Job time: 48.3268 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fischer RL, Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS96700
                                                                            WO200180626-A1.
Triticum sp.
                                                                                                                                                                 01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
```

ő

Tatarinova TV;

œ

The

```
The invention relates to an isolated polynucleotice at least 40% identical to DWT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or Complement encoding a polypeptide having a sequence at least 40% identical to DWT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C their compliations. Also included are an expression assette comprising the polyvuclectide or comprising a heterologus polynuclectide under the control of a promoter at least 70% identical to DWT 5' flanking sequence or an 5' untranslated ercoding a DWT-like protein. The expression cassette is polynuclectide encoding a DWT-like protein. The expression cassette is polynuclectide encoding a DWT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is cappalle of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of protein in a plant results in a delay in flowering time, introduction of chromosomal DNA in the cell, reduction of expression of the protein in a plant cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the DEMETER is related to 5-methylcytosine glycosylases and regulates

The polynucleotide is useful for detecting a nucleic acid in a sample. The DEMETER is related to 5-methylcytosine glycosylases and regulates
                                                                                                                                                                                                                                                                                                                                                           New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 TILVPCRTAMRGSFPLNGTYFQVNEVFADHRSSHNPIHVEREMLWNLQRRMVFFGTSVPT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 DPTPYLLAIWTP--DGIKEITKTPKPC--CDPQMGGDLCNNEMCHNCTAEKENQSRYVRG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1e-09;
0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 IFKGLRTEEIQQCFWRGFVCVRGFDMETRAPRPLCPHLH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 85; DB 23;
Pred. No. 1e-09;
                                                                                                                                                                                                                             Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 97; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU72754 standard; Protein; 209 AA.
                                                                                                                                                                                                                             Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.4%; 23.3%;
                                                     23-APR-2001; 2001WO-US13059.
                                                                                                             21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 23.3
Matches 37; Conservative
                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                          Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.
                                                                                                                                                                                                                                                                               WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AA;
                                                                                                                                                                                                                                                                                                               N-PSDB; AAS96714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soybean DMT3
                                                                                                                                                                                                                          Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2002
01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU72754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XX E XX E
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                        complement endoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or or their compliantions. Also included are an expression carsette comprising the polynucleotide or comprising a heterologues polynucleotide or comprising a heterologues polynucleotide comprising a heterologues polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exagence or an 5' untranslated region of DMT, a host cell comprising an exagence or an 5' untranslated comprised bMT-like protein. The expression cassette is polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following blological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of chromosomal DNA in the cell, reduction of expression of the protein in a harbidopsis leaf results in expression of the protein in a harbidopsis leaf results in expression of the protein in a harbidopsis leaf results in expression of the protein in a sample. DEMETER is related to 5-methyloytosine glycosylasses and requiates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                            New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
                                                                                                                                                                                                                                                                                                            invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 PCRTAMRGSFPLNGTYFQVNEVFADHCSSQNPIDVPRSWIWDLPRRTVYFGTSVPTIFRG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 YLLSIWTP-GETAQSIDAPKTFC---DSGETGRLCGSSTCFSCNNIREMQAQKVRGTLLI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                          Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87; DB 23; Length 164;
Pred. No. 3.5e-10;
0; Mismatches 112; Indels
                          Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 LXXXXIXXXFXXGXXCXRXFXXXXXXXXXX 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 LTTEEIQRCFWRGFVCVRGFDRTVRAPRAL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corn DMT protein related sequence #2.
                                                                                                                                                                                                                                                    Disclosure; Page 94; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU72764 standard; Protein; 179 AA.
                          Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 14.7%;
Local Similarity 22.7%;
nes 34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2002 (first entry)
                       Choi Y,
                                                                            WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 AA;
                                                                                                             N-PSDB; AAS96709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200180626-A1.
                       Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU72764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
```

Query Match Best Local &

Matches

ò g ò

ä

4; Gaps

Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;

Zea mays

RESULT 13 AAU72764

g

ò g

Length 179;

```
(REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU72759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU72759
   δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                     B
                                                                                                                                                                                                                                          cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of the protein into a cell results in modulation of free protein of cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present
                                                                                 complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or Cor their combinations. Also included are an expression cassette comprising the polymucleotide or comprising a heterologous polymucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polymucleotide encoding a DMT-like protein and a transgenic plant comprising a polymucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual
New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                       The invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 KXXXXLRTEHXVXXLPDXHXXLXXXDX-----XXYLLXIWXPXXXXXX----XXXXXX 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 KNVSRLRTEHCVYELPDTHPLLQGWDTREPDDPGKYLLAIWTPGETANSIQPPESKCSSQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 88.5; DB 23; Length 102;
Pred. No. 1e-10;
0; Mismatches 52; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 EEC-----GOLCNENECFSCNSFREANSQIVRGTLL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi Y, Hannon M, Okamuro JK,
                                          Disclosure; Page 91; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cotton DMT protein related sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU72760 standard; Protein; 137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.0%;
28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2001; 2001WO-US13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 28.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gossypium hirsutum.
                                                                                                                                                                                                                                                                                                                                                                                                                                       102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200180626-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU72760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
à
```

```
The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% and complement encoding a polypeptide having a sequence at least 40% or their combinations. Also included are an expression or their combinations. Also included are an expression or cassette comprising the polynucleotide or comprising a heterologous cassette comprising the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide condition and a transgenic plant comprising a cooling a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of chromosomal DNA in the cell, reduction of expression of the protein in a prabidospisal leaf results in expression of the protein in a prabidospisal leaf results in expression of the method or method or the protein in a protein in an Arabidospisal leaf results in expression of the method or method or the protein in a protein in an Arabidospisal leaf results in expression of the method or method or the protein in an Arabidospisal leaf results in expression of the method or metho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                        New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 KNVSRLRTEHYVYELPDKHPLLKQMEKREPDDPSPYLLAIWTP-GETANSIQPPEQSC-- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23; Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.7%; Score 87; DB 23;
29.8%; Pred. No. 2.9e-10;
tive 0; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 -GSQEPGRLCNEKTCFACNSVREANTETVRGTIL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corn DMT protein related sequence #1.
                                                                                                                                                                                                                                                                                                                      Disclosure; Page 94; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU72759 standard; Protein; 164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2000; 2000US;0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Demeter; DMT; Atrop
DNA demethylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 AA;
                                       N-PSDB; AAS96710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-2001
```

a

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                             Db
                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                          3;
                                                              The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                 1166 ALFESNNTLCNENKCFQCNKTREEESQTVRGTILIPCRTAMRGGFPLNGTYFQTNEVFAD 1225
                                                                                                                                                                                                                                                                      1109 KIKEKLRTEHHVFELPDHHSILEGFERREAEDIVPYLLAIWTP-GETVNSIQPPKQRC-- 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40%
                                                                                                                                                                                                                                                                                            104 KXXXXLRTEHXVXXLPDXHXXL-----XXXDXXXYLLXIWXPXXXXXXXXXXXXXX 157
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                          ٠.
ف
                                                                                                                                                                                                     DB 23; Length 1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DMT; Atropos; ATR; 5-methylcytosine glycosylase;
thylation; transgenic plant; transcription modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tatarinova TV;
                                           Claim 5; SEQ ID NO 1471; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                             HDSSINPIDVPTELIWDLKRRVAYLGSSVSSICKGLSVEAIKYNFQEG 1273
                                                                                                                                                                                                                                                                                                                                        Score 108.5; DB 23;
Pred. No. 7.6e-14;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 84; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAU72745 standard; Protein; 177 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Σ̈́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hannon
                                                                                                                                                                                                    18.4%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2002 (first entry)
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-055307/07.
                                                                                                                                                                              1309 AA;
                                                                                                                                                                                                            Local Similarity
nes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        demethylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corn DMT1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS96696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fischer RL,
                       organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU72745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Demeter;
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                             1226
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
Ġ
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                        ç
                                                                                                                                                                                                                                                                                                                                                            엄
```

```
cross, and selecting a host cell with modulated transcription. Where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylatycosine glycosylases and regulates transcription of target genes by demethylation. The present
                         or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual
identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 PCRTAMRGSFPLNGTYFQVNEVFADHCSSQNPIDVPRSWIWDLPRRTVYFGTSVPTIFRG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 YLLSIWTP-GETAQSIDAPKTFC---DSGETGRLCGSSTCFSCNNIREMQAQKVRGTLLI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB 23; Pred. No. 6.3e-13; 0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU72755 standard; Protein; 102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.9%;
23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2001; 2001WO-US13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 23.8
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS96705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soybean DMT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU72755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
```

.; ;

S

```
WO200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tietjen K,
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB92260;
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
   В
                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates sequence represents a DMT-like protein. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, or C or their combinations. Also included are an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a sequence
                                                                                                                                                                                                                                                                                                      HETSLNPIVERRELCKGLEKRALYCGSTVTSIFKLLDTRRIELCFWTGFLCLRAFDRKQR 1051
                                                                                                                                                                                       KYYNRLRIEHVVYVLPDNHELLHDFERRKLDDPSPYLLAIWQP-GETSSSFVPPKKKC-- 955
                                                                                                                                                                                                                                    DB 23; Length 1114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide that control plant development having a specific homology to DEMETER domains A,B
                                                                                                                                                                0; Mismatches 108;
                                                                                                                                                                                                                                                          --SSDGSKLCKIKNCSYCWTIREONSNIFRGTIL-----
                                                                                                                                          Score 134.5; DB : Pred. No. 1.8e-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomato DMT protein related sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 92; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              AAU72757 standard; Protein; 210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi Y, Hannon M,
                                                                                                                                         ch 22.8%;
1 Similarity 25.8%;
49; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2001; 2001WO-US13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                     1052 DPKELVRRLH 1061
                                                                                                                                                                                                                                                                                                                               278 XPXXLXXXLH 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-055307/07.
                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS96707
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU72757:
                                                                                                                    Sequence
                                                                                                                                          Query Match
                                                                                                                                                                                                             899
                                                                                                                                                                                                                                                                                 218
                                                                                                                                                                                                                                                                                                        992
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
  $$$$$$$$$$$$$$$
                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                       g
```

```
.;
cassette comprising the polynucleotide or comprising a heterologous bolynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of the chromosomal DNA in the cell, reduction of expression of the protein in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 KXXXXLRTEHXVXXLPDXHXXLXX-----XDXXXYLLXIWXPXXXXXX----XXXXXXX 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DC-----GOLCNEEECFSCNSFREANSQIVRGTILIPCRTAMRGSFPLNGTYFQVNE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 VFADHESSLNPISVPRSLIWNLDRRTVHFGTSVTSIFKGLATPEIQQCFWRGFVCVRSFE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying plant target proteins for herbicidally active compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 KNVSRLRTEHSVYELPDSHPLLEGWEKREPDDPGKYLLAIWTPGETANSIQPPDRRCSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 132; DB 23;
Pred. No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herbicidally active polypeptide SEQ ID NO 1471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB92260 standard; Protein; 1309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.48; 24.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weldler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 XXXXXPXXL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 RSTRAPRPL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER AG.
```

us-09-840-743-73.rag

Sat Nov

```
The invention relates to an isolated polynuclectide sequence or their complement encoding a polypeptide having a sequence at least 40% complement encoding a polypeptide having a sequence at least 40% complement encoding a polynucled, who was a RTRODGS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynuclectide or comprising a heterologous composition of DMT, a host cell comprising an exogenous polynuclectide to DMT, a host cell comprising an exogenous polynuclectide casoling a DMT-like protein and a transgenic plant comprising a composition a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing cost, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following cross, and selecting a host cell with modulated transcription of the protein in a plant results in a delay in flowering time, introduction of the protein in a plant results in a delay in flowering time, introduction of the protein in a plant cell, reduction of expression of the protein in a plant cell, reduction of expression of the protein in an Arabidopsis leaf results in modulation of methylation of plant in a plant results in modulation of expression of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynuclectide is useful for detecting a nucleic acid in a sample. ComeMETER is related to 5-methylcytosine glycosylases and regulates composition of purpose by demethylation. The present regulates a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
  DC-----GQLCNEEECFSCNSFREANSQIVRGTILIPCRTAMRGSFPLNGTYFQVNE 139
                                          140 VFADHESSLNPISVPRSLIWNLDRRTVHFGTSVTSIFKGLATPEIQQCFWRGFVCVRSFE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                               Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okamuro JK, Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 71; 109pp; English.
                                                                                                                                                                                                                                                                             AAU72739 standard; Protein; 1332 AA
                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis DMT3 (1DMT3) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000; 2000US-0553690
                                                                                                                          274 XXXXXPXXLXXXLHXXXS 291
                                                                                                                                                                      200 RSTRAPRPLMARLHFPAS 217
                                                                                                                                                                                                                                                                                                                                                             26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fischer RL, Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis Thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-055307/07.
N-PSDB; AAS96693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                     AAU72739;
88
                                                                                                                                                                                                                                                                           g
                                          ò
                                                                                  g
                                                                                                                            δ
                                                                                                                                                                  g
```

```
The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMPTER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' lanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the
                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                          1132 KIKEKLRTEHHVFELPDHHSILEGFERREAEDIVPYLLAIWTP-GETVNSIQPPKORC-- 1188
                                                                                                                                                                                    1189 ALFESNNTLCNENKCFOCNKTREEESQTVRGTILIPCRTAMRGGFPLNGTYFOTNEVFAD 1248
                                                                                                                                                                                                                                                            1249 HDSSINPIDVPTELIWDLKRRVAYLGSSVSSICKGLSVEAIKYNFQEGYVCVRGFDRENR 1308
                                                                         Length 1332;
                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okamuro JK, Tatarinova TV;
                                      Indels
                                    132;
Score 137.5; DB 2
Pred. No. 4.8e-20;
); Mismatches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU72741 standard; Protein; 1114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 75; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis DMT4 (1DMT4) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hannon M,
                                      ;
0
 23.3%; 25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fischer RL, Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis Thaliana.
                                                                                                                                                                                                                                                                                                                                      1309 KPKSLVKRLH 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-055307/07.
                                                                                                                                                                                                                                                                                                   278 XPXXLXXXLH 287
                     Best_Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS96694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200180626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU72741;
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            AAU7274
                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                      Dp
                                                                                                                                                                                                                                                              СP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Óγ
                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                     δλ
```

Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.

Medicago sativa. WO200180626-A1.

Alfalfa DMT protein related sequence.

(first entry)

26-FEB-2002

AAU72756;

AAU72756 standard; Protein; 217 AA.

```
AAU72756
                                              The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% dentical to DMT (DEMPTER, previously known as ATROPOS (ATR)) Domain A, B control to their combinations. Also included are an expression assette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5. flanking sequence, DMT 3. flanking sequence or an 5. untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual the protein is capable of exhibiting at least one of the following bloological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of plant results in a delay in flowering time, introduction of plant results in enhanced endosperm development and expression of the protein in a Arabidopsis leaf results in expression of the protein in a plant result for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. The company capages and regulates are appreased to seminate a part of the protein of terraget genes by demethylation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                       New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1745 KNVSRLRTEHQVYELPDSHPLLEGFNQREPDDPCPYLLSIWTP-GETAQSTDAPKSVC-- 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 KXXXXXLRTEHXVXXLPDXHXXLXX-----XDXXXYLLXIWXPXXXXXXXXXXXXXXXX 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 10;
DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 145; DB 23; Length 1952;
Pred. No. 1.8e-21;
0; Mismatches 134; Indels 10
                                                                                                                                                                                                                   Okamuro JK, Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 79-80; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents a DMT-like protein
                                                                                                                                                                                                                    Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.6%;
26.2%;
                                                                                                                              23-APR-2001; 2001WO-US13059.
                                                                                                                                                          21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 26.2 ies 51; Conservative
                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                   Choi Y,
                                                                                                                                                                                                                                             2002-055307/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1952 AA;
                                                                                                                                                                                                                                                           N-PSDB; AAS96695
                                                                       WO200180626-A1.
                                           Oryza sativa.
                                                                                                  01-NOV-2001.
                                                                                                                                                                                                                   Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
```

New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or  ${\tt C}$ 

Disclosure; Page 92; 109pp; English.

Okamuro JK, Tatarinova TV;

Hannon M,

N-PSDB; AAS96706

(REGC ) UNIV CALIFORNIA Fischer RL, Choi Y, 2002-055307/07.

23-APR-2001; 2001WO-US13059. 21-APR-2000; 2000US-0553690.

01-NOV-2001

```
The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a condulating a pMT-like protein. The expression cassette is confound a DMT-like protein. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following brotein in a plant results in addition of methylation of the protein in a plant results in a modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in expression of the model of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ë.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 KXXXXLRTEHXVXXLPDXHXXLXX-----XDXXXYLLXIWXPXXXXXX----XXXXXXX 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 KNVSRLRTEHSVYELPDSHPLLEGWEKREPDDPGKYLLAIWTPGETANSIQPPDRRCSAQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.2%; Score 143; DB 23; Length 217; 25.3%; Pred. No. 4.9e-22; Live 0; Mismatches 130; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a DMT-like protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ry ....st Local S.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

1802 -NSQENGELCASNTCFSCNSIREAQAQKVRGTLLIPCRTAMRGSFPLNGTYFQVNEVFAD 1860

à q ò g à 1861 HDSSRNPIDVPRSWIWNLPRRTVYFGTSIPTIFKGLTTEEIQHCFWRGFVCVRGFDRTSR 1920

1921 APRPLYARLHFPASK 1935

278 XPXXLXXXLHXXXSK 292

Tatarinova TV;

Okamuro JK,

~

```
complement encoding a polypeptide having a sequence at least 40% of complement encoding a polypeptide having a sequence at least 40% of complement encoding a polypeptide having a sequence at least 40% of core for their complements. Also included are an expression cassette comprising the polynucledide or comprising a heterologous cassette comprising the control of a promoter at least 70% identical to polynucleotide under the control of a promoter at least 70% identical to comprise in sequence. Dary a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a compliant and a transgenic plant comprision cassette is polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following to protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of the protein into a new plant results in modulation of methylation of the protein in an Arabidopsis leaf results in expression of the MEDRA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. The DEMETER is related to 5-methylcytosine glycosylases and regulates construction of transcription of tearget genes by demethylation. The present
                                                                                                                                                                                                                                                                New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1214 KNISQLRTEHRVYELPDEHPLLAQLEKREPDDPCSYLLAIWTP-GETADSIQPSVSTC-- 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1271 -IFQANGMLCDEETCFSCNSIKETRSQIVRGTILIPCRTAMRGSFPLNGTYFQVNEVFAD 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1330 HASSLNPINVPRELIWELPRRTVYFGTSVPTIFKGLSTEKIQACFWKGYVCVRGFDRKTR 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide sequence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.6%; Score 145; DB 23; Length 1.
26.2%; Pred. No. 1.3e-21;
Live 0; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 67; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU72743 standard; Protein; 1952 AA.
                                                                                                                        Hannon M,
21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1390 GPKPLIARLHFPASK 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 XPXXLXXXLHXXXSK 292
                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                     Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 51; Conserve
                                                                                                                                                                                 WPI; 2002-055307/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice DMT1 protein.
                                                                                                                                                                                                          N-PSDB; AAS96692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2002
                                                                                                                     Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU72743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                               The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a condulating a DMT-like protein and a transgenic plant comprising a condulating a polynucleotide encoding a DMT-like protein. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium of the following bloogical activities, which include enhanced expression of the protein in a plant results in a doublation of methylation of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. Content of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. Content of the protein in an Arabidopsis by demethylation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1590 -GGKASGKMCFDETCSECNSLREANSQTVRGTLLIPCRTAMRGSFPLNGTYFQVNELFAD 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1533 KNISRLRTEHQVYELPDSHRLLDGMDKREPDDPSPYLLAIWTP-GETANSAQPPEQKC-- 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1649 HESSLKPIDVPRDWIWDLPRRTVYFGTSVTSIFRGLSTEQIQFCFWKGFVCVRGFEQKTR 1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 KXXXXLRTEHXVXXLPDXHXXLXXXXX-----XXYLLXIWXPXXXXXXXXXXXXXXX 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 146; DB 23; Length 1729;
Pred. No. 9.6e-22;
0; Mismatches 134; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a DMT-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU72737 standard; Protein; 1413 AA.
                               Claim 3; Page 54-55; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis DMT2 (1DMT2) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 24.7%;
Local Similarity 26.2%;
les 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-2001; 2001WO-US13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1709 APRPLMARLHFPASK 1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 XPXXLXXXLHXXXSK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis Thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1729 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200180626-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU72737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
```

AAU72737

ò g ò

ò g 3;

Length 1413;

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

2002, 19:24:08; Search time 45.3268 Seconds (without alignments) 858.415 Million cell updates/sec ъ Э November Run on:

US-09-840-743-73 590

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters: Searched:

908470

length: 0 length: 2000000000 DB seq I Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_101002:* Database

/SIDS2/gcgdata/geneseq/genesegp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/genesegp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqgenesegp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqgp-embl/AA1982.DAT:*/SIDS2/gcgdata/genesegg-embl/AA1983.DAT:*/SIDS2/gcgdata/genesegg-embl/AA1983.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1984.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1988.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1988.DAT:*

/SIDS/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
/SIDS/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
/SIDS/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
/SIDS/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
/SIDS/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
/SIDS/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
/SIDS/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
/SIDS/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
/SIDS/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
/SIDS/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:* /SIDS2/gcgdata/geneseg/genesegp.embl/AA1999.DAT:*/SIDS2/gcgdata/geneseg/genesegp.embl/AA2000.DAT:*/SIDS2/gcgdata/geneseg/genesegp.embl/AA2001.DAT:*/SIDS2/gcgdata/geneseg/genesegp.embl/AA2001.DAT:*/SIDS2/gcgdata/geneseg/genesegp.embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Arabidosis Demete	Arabidopsis DMT2 (	Rice DMT1 protein.	Alfalfa DMT protei	Arabidopsis DMT3 (	Arabidopsis DMT4 (	Tomato DMT protein	Herbicidally activ	Corn DMT1 protein.	Soybean DMT4 prote
SUMMARIES			ID	AAU72736	AAU72737	AAU72743	AAU72756	AAU72739	AAU72741	AAU72757	ABB92260	AAU72745	AAU72755
			DB	23	23	23	23	23	23	23	23	23	23
			Match Length DB ID	1729	1413	1952	217	1332	1114	210	1309	177	102
	dР	Query	Match	24.7	24.6	24.6	24.2	23.3	22.8	22.4	18.4	16.9	15.0
			Score	146	145	145	143	137.5	134.5	132	108.5	100	88.5
		Result	No.	T	7	m	4	S	9	7	80	6	10

Cotton DMT protein Corn DMT protein r	Corn DMT protein r	an DM	Wheat DMT3 protein	Corn DMT protein r		Corn DMT protein r	Corn DMT protein r	Corn DMT protein r	Wheat DMT1 protein	. Corn DMT protein r	phil	UGGT. Drosophila	Drosophila cell cy	Human peptidase, H	Human PRO4389 poly	Human digestive sy	Human colorectal c	Drosophila melanog	Human immune/haema	Zea mays protein f	Propionibacterium	Cosmid cHRIMS enco	Propionibacterium	Propionibacterium	E. rhusiopathiae s	Drosophila melanog	Arabidopsis thalia	Human prostate can	Human reproductive	Arabidopsis thalla	Arabidopsis thalia	Human HOMO tyrosin	Human transport pr
AAU72760 AAU72759	AAU72764	AAU72754	AAU72750	AAU72766	AAU72767	AAU72765	AAU72768	AAU72769	AAU72748	AAU72770	ABB62738	AAB72443	AAM47583	AAY90301	AAU12260	AAM92597	AAM38606	ABB66499	AAM88162	AAG35357	AAU50869	AAY95685	AAU48812	AAU53845	AAY43219	ABB70840	AAG27372	AAU22769	AAM94749	AAG06711	AAG06710	AAU10493	AAB60106
23	23	23	23	23	23	23	23	23	23	23	22	22	23	21	22	22	22	22	22	21	22	21	22	22	20	22	21	22	22	21	21	23	22
137	179	209	108	140	138	150	68	93	183	71	1548	1548	1548	229	229	233	233	3503	82	144	204	662	75	81	909	1289	49	83	83	109	112	152	154
14.7		13.4	13.1	13.1	12.9	12.5	12.2	11.2	10.0	9.5	6.9	6.9	6.9	6.3	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	5.9	5.9	5.9	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8
87	85	79	77	11	16	74	72	99	59	54	41	41	41	37	37	37	37	37	36	36	36	36	35	35	35	34.5		34	34	34	34	34	34
111	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA. AAU72736 standard; Protein; 1729 AA 23-APR-2001; 2001WO-US13059. Arabidopsis Demeter protein 26-FEB-2002 (first entry) Arabidopsis Thaliana WO200180626-A1. 01-NOV-2001. AAU72736; RESULT 1 

21-APR-2000; 2000US-0553690. (REGC ) UNIV CALIFORNIA.

Tatarinova TV; Okamuro JK, Fischer RL, Choi Y, Hannon M,

WPI; 2002-055307/07. N-PSDB; AAS96686, AAS96689.

New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C  $\,$ 

THIS PAGE BLANK (USPTO)

;

```
| REFERENCE/DOCKET NUMBER: DX0335K1 | TELECOMMUNICATION INFORMATION: | TELECOMMUNICATION INFORMATION: | TELECHONE: 415-496-1206 | TELECHONE: 415-496-1206 | TELECHONE: 415-496-1200 | TELECHON: 15-496-1200 | TELECHOR: 415-496-1200 | TYPE: amino acids | TYPE: aci
```

Search completed: November 8, 2002, 19:29:22 Job time: 22.6993 secs

ó

```
APPLICANT: Moore, Kevin W.
APPLICANT: Liu, Ying
APPLICANT: Liu, Ying
APPLICANT: Hou, Alice Suk-Yue
APPLICANT: Hou, Alice Suk-Yue
APPLICANT: Bazan, Ji-Hwei
APPLICANT: Bazan, Ji-Hwei
APPLICANT: Tan, Jimmy C.
APPLICANT: Tan, Jimmy C.
APPLICANT: Chou, Chuan-Chu
TITLE OF INVENTION: (IL-10)
NUMBER OF SEQUENCES: (IL-10)
NUMBER OF SEQUENCES: ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUWTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 1; Length 578;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,788
FILING DATE: 19-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0501
TELECOMMUNICATION INFORMATION:
TELECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,683
FILING DATE: 23-AUG-1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/011,066
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08110683
Patent No. 5789192
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 578 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-788-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 LOTEEPOFLLPDPH 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-110-683-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                  APPLICANT: Moore, Kevin W.
APPLICANT: Wei, Sherry
APPLICANT: Ho, Alice Suk-Yue
TITLE OF INVENTION: MAMMALIAN INTERLEUKIN-10 (IL-10)
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Moore, Kevin W.
APPLICANT: Wel, Sherry
APPLICANT: Ho, Alice Suk-Yue
TITLE OF INVENTION: MAMMALIAN INTERLEUKIN-10 (IL-10)
TITLE OF INVENTION: SUPER-ACTIVATING RECEPTORS; AND VARIANTS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME:

CLASSIFICATION NUMBER:

ATTORNEY/AGENT NIFORMATION:

NAME:

REGISTRATION NUMBER:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE:

415.852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Le
Pred. No. 1.6e+02;
1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-424-788-5; Sequence 5, Application US/08424788; Patent No. 5716604; GENERAL INFORMATION:
                                                                                                                                                                                                              Sequence 6, Application US/08424788 Patent No. 5716804 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.4%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-788-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 LOTEEPQFLLPDPH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
133 YLLXIWXP 140
                                   ||| :| |
976 YLLSLWPP 983
                                                                                                                                                    RESULT 13
US-08-424-788-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
ò
                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/09170996

Patent No. 6291220
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Chen, Yen-Wen
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 6291220e1 PI 3-Kinase Polypeptides
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 4; Length 1876;
Pred. No. 3.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                     Length 1876;
                                                                                                                                                                                                                                                                                                                                     Score 33; DB 4; Length 187
Pred. No. 3.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-063700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2442
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2307K-063700US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PROG APPLICATION DATA:
APPLICATION NUMBER: US 08/609,049
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                       5.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.6%;
29-FEB-1996
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.5%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two EmecaCITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-170-996-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  133 YLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                         976 YLLSLWPP 983
  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-170-996-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-170-996-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                    ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
        MOLY, Lisa
Chen, Yen-Wen
Chen, Yen-Wen
WENTION: No. 5948664el PI 3-Kinase Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Williams, Lewis T.
APPLICANT: Mol2, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STREE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2; Length 15,7
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,049A
FILING DATE: 29-FEB 1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: DOW, KATON B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 23,07K-063700US
TELEPAMINICATION INFORMATION:
TELEPAMINICATION INFORMATION:
TELEPAMINICATION SEQUENCE: 415-326-240
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 emino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,996
                                                    TITLE OF INVENTION: No. 5948664el PI 3-Kina:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09170996
Patent No. 6291220
Williams, Lewis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.6%;
                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.5
                                                                                                                                  STREET: Two Embarcade
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-609-049A-28
                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 YLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| :| |
976 YLLSLWPP 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-170-996-12
APPLICANT:
                                      APPLICANT:
```

op • δ

Gaps

ö

```
APPLICANT: Williams, Lewis T.
APPLICANT: Wolz, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                    Length 1839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 2; Length 187
Pred. No. 3.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA: US/08/609,049A
FILING DATE: 29-FEB-1996
                                                                                                                                                      Score 33; DB 2; 1
Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFTLING DATE: 29-FEB-1990
CLASSIFICATION: 435
ATTORNEY/ABENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111.3834
COMPUTER REARABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08609049A; Patent No. 5948664; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/08609049A; Patent No. 5948664; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE DOCKET NUMBER: 230
TELECOMUNICATION INFORMATION:
TELEBHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.6%;
                                                                                                                                                      5.6%;
                                                                                                                                        Query Match
Best Local Similarity 60.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.6
Best Local Similarity 62.5
Matches 5; Conservative
                                                                            ; FEATURE: -
; OTHER INFORMATION: 929491
US-09-172-977-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Embarcac
CITY: San Francisco
STATE: California
                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                       1493 DOSQYLLKIW 1502
                                                                                                                                                                                                                               129 DXXXYLLXIW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 YLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| :| |
976 YLLSLWPP 983
                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-609-049A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-609-049A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-609-049A-12
    SEQ ID NO 4
LENGTH: 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                            Sequence 2, Application US/08899514

Patent No. 5910581

GENERAL INFORMATION:
APPLICANT: HABUCHI OSAMI
APPLICANT: FUKUTA, MASARAZU
TITLE OF INVENTION: SULFOTRANSFERASE ORIGINATING FROM HUMAN AND DNA CODING
TITLE OF INVENTION: FOR THE POLYPEPTIDE
OUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 479;
                                                                                                                                                                                                                                                                                                           ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR, LLP
STREET: 620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: We, Henry
ITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
FILE REFERENCE: PP-0615 US
CURRENT APPLICATION UNMBER: US/09/172,977
CURRENT APPLICATION OF A NUMBER: US/09/172,977
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.6%; Score 33; DB 2;
45.5%; Pred. No. 82;
ative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOYAM21.001AUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,514
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09172977
Patent No. 5989863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: DANIELE ALTMAN
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: TOY.
TELECHMONIC, 714 760 9404
TELEPHONE: 714 760 9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 714 760 9502 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-899-514-2
                                                                                                                                                                                                                                                                                                                                                CITY: NEWPORT BEACH STATE: CALIFORNIA
60 DTNRYLADVWVP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Local 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 : 11: 1
204 EHFITPLPEDH 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 EHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-172-977-4
                                                                                            US-08-899-514-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ö

Gaps

```
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                    129 DXXXXLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 DXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                     41 DTNRYLADVWVP 52
                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USID: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-071-035-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Baltz, Richard H

APPLICANT: Baltz, Richard H

APPLICANT: Baltz, Richard H

APPLICANT: Broughton, Mary C

APPLICANT: Madduri, Kishnamurthy

APPLICANT: Treadway, Parti J

APPLICANT: Treadway, Parti J

APPLICANT: Waldron, Clive

TITLE OF INVENTION Biosynthetic Genes For Spinosyn Insecticide

FILE REFERENCE: 50489 DIVI

CURRENT APPLICATION NUMBER: US/09/36987

EARLIER APPLICATION NUMBER: US 09/36987

EARLIER FILING DATE: 1998-03-09

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 22

LENTH: 278
                                                                              0
                                   Score 34; DB 4; Length 278;
Pred. No. 29;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%; Score 34; DB 4; Length 278; 50.0%; Pred. No. 29; tive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOGTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT : ORGANISM: Saccharopolyspora spinosa US-09-370-700-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 76, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
                                                                                                                                                                                                                                             Sequence 22, Application US/09370700 Patent No. 6274350
                                     5.8%;
                   Query Match
Best Local Similarity 50.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.8
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                               109 LRTEHXVXXLPDXH 122
                                                                                                                                                   159 LNTEQUVAILPTSH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 LNTEQUVALLPTSH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
US-09-036-987A-22
                                                                                                                                                                                                          RESULT 4
US-09-370-700-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5 .
US-109-071-035-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ογ
                                                                                                                 ò
```

```
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVORTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                              Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 4;
Pred. No. 20;
1; Mismatches (
                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                              Score 33; DB Pred. No. 17; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
                                         PB369P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 74, Application US/09071035; Patent No. 6448043
                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 74
                                                                                                                                                                                                                                                                                                            Query Match 5.6%;
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           single
                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-09-071-035-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-071-035-74
```

```
MOLECULE TYPE: protein
     PAGES: 126-133
DATE: 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-036-987A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                        JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                        US-08-685-466C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: P. Moretti, G. Hintermann, R. H tter
TITLE: Isolation and characterization of an
TITLE: extrachromosomal element from No. 6015705ardia mediterranei
JOURNAL: Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
AUTHORS: G.J.W. Euverink, D.J. Wolters, L.
AUTHORS: Dijkhuizen
TITLE: Prephenate dehydratase of the actinomycete
TITLE: Amycolatopsis methanolica: purification and
TITLE: characterization of the wild-type and deregulated mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: G.J.W. Euverink, G.I. Hessels, J.W. AUTHORS: Vrijbloed, J.R. Coggins, L. Dilkhuizen
TITLE: Purification and characterization of a dual
TITLE: function 3-hydroquinate dehydratase from Amycolatopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified amino acid, formylmethionine LOCATION: The first amino acid in the sequence, LOCATION: described as methionine, is actually known as LOCATION: formylmethionine ("fMet"). Polypeptide chains in LOCATION: bacteria often start with formylmethionine.

PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: L. de Boer, W. Harder, L. Dijkhuizen
TITLE: Phenylalanine and tyrosine metabolism in the
TITLE: facultative methylotroph No. 6015705ardia sp. 239
VOLUME: Arch. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: J. Cairns, J. Overbaugh, S. Miller
                                                                COMPUTER: Compag Prolines 5100
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wondperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,466C
FILING DATE: 24-JUL-96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,381
FILING DATE: 24-JUL-95
ATTORNEY/AGENT INFORMATION:
NAME: Dan.4el J. Hulseberg
REGISTRATION NUMBER: 36,554
REFERENCE/DOCKET NUMBER: 36,554
REDECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL: J. Gen. Microbiology
VOLUME: 138
PAGES: 2449-2457
ZIP: 60603-2828
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (312) 701-8606
TELEFAX: (312) 701-711
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 192 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methanolica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL: Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAGES: 142-145
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAGES: 459-465
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE: ch
TITLE: en
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Turner, Jan R.
TITLE OF INVENTION: Production
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
PUBLICATION INFORMATION:
AUTHORS: J. Sambrook, E.F. Frisch, T. Maniatis
TITLE: Molecular cloning: a laboratory manual
JOURNAL: Cold Spring Harbor Laboratory Press
DATE: 1989
PUBLICATION INFORMATION:
AUTHORS: J.W. Vrijbloed, J. Madon, L. Dijkhuizen
TITLE: A plasmid from the methylotrophic
TITLE: actinomycete Amycolatopsis methanolica capable of site-
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.8%; Score 34; DB 3; Length 192; Best Local Similarity 24.1%; Pred. No. 20; Matches 7; Conservative 3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dow AgroSciences LLC Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 RTEHXVXXLPDXHXXLXXXDXXXYLLXIW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 REEHHTVWFPPVAMAIVFNDTADHVLMAW 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/09/036,987A
09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09036987A Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dow AgroSciences L
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 278 amino acids TYPE: amino acid
                                                                                                                                                                                                                                J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 09-MAR
                                                                                                                                                                                                                                                                        VOLUME: 176
PAGES: 7087-7090
DATE: 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
```

```
Sequence 15, Appl Sequence 2, Appl Sequence 22, Appl Sequence 24, Appl Sequence 27, Appl Sequence 28, Appl Sequence 12, Appl Sequence 12, Appl Sequence 28, Appl Sequence 2, Appl Sequence 6, App
                                                                                          8, 2002, 19:24:15; Search time 16.6993 Seconds (without alignments) 514.481 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                         262574
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-815-718-3
US-08-206-006-2
US-09-134-001C-5040
US-08-884-072-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-376-330-15
US-08-685-466C-4
US-09-370-700-22
US-09-370-700-22
US-09-071-035-76
US-08-09-514-2
US-08-172-977-4
US-08-109-049A-12
US-09-170-996-12
US-09-170-996-12
US-08-424-788-5
US-08-437-166-2
US-08-437-166-2
US-08-439-672-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-928-612-3
US-09-199-637A-215
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-US93-11638-2
                                                                                                                                                                                                                                                                        262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ........
                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                              OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                          Searched:
                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002221009876543
20022210987654321009876543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
```

Sequence 6, Appli Sequence 404, App Sequence 402, App Sequence 8, Appli Sequence 8, Appli Sequence 9, Appli Sequence 20, Appli Sequence 10, Appl Sequence 11, Appl		osyltransferase (UGGT) activity UGGT	Length 1548; ; Indels 0; Gaps 0;		Dijkhuizen DNA of an Method of Detection and Andifying the DNA of an Comprising Modified DNA
US-09-212-168-6 US-09-071-035-404 US-09-071-035-402 US-08-144-926A-8 US-08-926-922-8 US-09-253-682-8 US-09-247-737-20 US-09-247-77-20 US-09-134-001C-4141 US-09-134-001C-4141 US-08-943-714-12 US-08-943-714-12 US-08-943-714-12 US-09-627-650B-11 US-08-469-260A-81 US-09-436-063C-11 US-09-436-063C-11	ALIGNMENTS	Guence 15, Application US/09376330 Sequence 15, Application US/09376330 Sequence 15, Application US/09376330 SENERAL INFORMATION: APPLICANT: Tessier, Daniel C. APPLICANT: Dignard, Daniel C. APPLICANT: Dignard, Daniel C. APPLICANT: Begeron, John J.M. APPLICANT: Homes, David Y. TITLE OF INVENTION: Wethod for screening for TITLE OF INVENTION: WDP-glucose;glycoprotein glucosyltransferase TITLE OF INVENTION: WDP-glucose;glycoprotein glucosyltransferase FILE REFERENCE: 2139-9"US" CURRENT PAPLICATION NUMBER: US/09/376,330 CURRENT PAPLICATION NUMBER: US/09/376,330 CURRENT FILING DATE: 1999-08-18 NUMBER OF SEQ ID NOS: 35 LENGTH: 1548 TYPE: PRT ORGANISM: Artificial Sequence FRATURE: OTHER INFORMATION: D. melanogaster UGGT	Score 41; DB 4; Pred. No. 5.1; 2; Mismatches 26	PXXXXXXXKXXXLPEHXVXXLPDXHXXLXXXDXXXYL 134	and Lubbert difying the difying the A Sequence, a Gene Cap Organisms
559 1416 4 1448 4 175 1 175 2 175 3 175 3 175 4 219 4 315 4 310 4 1128 4 1128 4 1128 4 1152 4 1652 4		SGULT 1  -09-376-330-15  Sequence 15, Application US/09376330  Patent No. 6399321  APPLICANT: Dignard. Daniel APPLICANT: Dignard, Daniel APPLICANT: Tessier, Daniel APPLICANT: Thomas, David Y. TITLE OF INVENTION: Method for scre TITLE OF INVENTION: Method for scre TITLE OF INVENTION: Method for scre TITLE OF INVENTION: Method for SCIENTERE FINVENTION: Method for SCIENTER OF INVENTION: UDP-91ucose;91; TITLE OF INVENTION: UDP-91ucose;91; TITLE OF INVENTION: Method for SCIENTER OF SEQ ID NOS: 35 CURRENT APPLICATION NUMBER: US/09/3 CURRENT FILING DATE: 1999-08-18 NUMBER OF SEQ ID NOS: 35 SSOTWARE: FastSEQ for Windows Versit SSOTU NO 15 LENGTH: 1548 TYPE: PRT TYPE: TYPE: PRT TYPE: TYPE: PRT TYPE:	6.9%; larity 28.2%; Conservative	XLRTEHXVX)  : :    DLKTDHSVVK	SULT 2 Sequence 4, Application US/08685466C Patent No. 6015705 GENERAL INFORMATION: APPLICANT: Jan Willem Vrijbloed TITLE OF INVENTION: Method of MO TITLE OF INVENTION: Organism, DN TITLE OF INVENTION: Organism, DN TITLE OF INVENTION: Organism and NUMBER OF SEQUENCES: ADDRESSEE: Daniel J. Hulseberg STREET: P.O. BOX 2828 CITY: Chicago STATE: IL
		330-15 15, Applica: 10.6.399321 10.6.6393231 INT: Tessier, INT: Dignard INT: Bergero INT: Persero INT: Perser	Ë	XXXXKXXX.         KTRFKLPT	4, Application 1, 6015705 1, 1NFOWATION: ANT: Jan Wille OF INVENTION: OF INVENTION: OF INVENTION: OF INVENTION: OF SEQUENCES FROM SEGUENCES F
2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		Sequence 15, Applications of the control of the con	Matc Local	96 PXXX       935 PRQT	Sulr 2 Sequence 4, Application U Sequence 4, Application U Patent No. 6015705 GENERAL INFORMATION: APPLICANT: Jan Willem TITLE OF INVENTION: M TITLE OF INVENTION: I STREET: P.O. BOX 28: CORRESPONDENCE ADDRESS ADDRESSEE: Daniel J STREET: P.O. BOX 28: CITY: Chicago
44444444444444444444444444444444444444		RESULT US-09- Sequ Sequ APP APP APP APP APP APP APP APP APP AP	Query Best Match	QV Db	RESULT 2 US-08-681 Sequence Patent GENERY TITI TITI TITI TITI TITI TITI TITI TI

THIS PAGE BLANK (USPTO)

```
R FILING DATE: 1998-06-04

R PAPLICATION WHBER: 60/088028

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088029

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

R FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085573
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
                                                FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
                                                                                                                                  APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/083322
                                                                                                                                                                                                                                                                                    FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084114
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-05-15
APPLICATION UNDHER: 60/085700
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/086023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/086486
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/087098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087208
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
                                                                                                                                                                                                      60/083495
                                                                                                                                                                                                                                     60/083496
                                                                                                                                                                                                                                                                      60/083499
                                                                                                                                                                                                                                                                                                                                       60/084366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60/085580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088025
                                 APPLICATION NUMBER: 60/082568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/086392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
                                                                                                   APPLICATION NUMBER: 60/082704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/088167
                                                                                                                                                                                 FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/0
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/0
                                                                                                                                                                                                                                                       1998-04-29
                                                                                                                                                                                                                                                                                                                       1998-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/0
                                                                                                                    1998-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLING DATE: 1998-05-18
                                                                                                                                                                                                                                                     FILING DATE: 1998-04 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-04
APPLICATION NUMBER:
                                                                                                                  FILING DATE:
               PRIOR
```

PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/08855
PRIOR APPLICATION NUMBER: 60/08855
PRIOR APPLICATION NUMBER: 60/08855
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR PRILOR APPLICATION NUMBER: 60/08811
PRIOR APPLICATION NUMBER: 60/08811
PRIOR APPLICATION NUMBER: 60/08824
PRIOR PILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11
PRIOR PELICATION NUMBER: 60/08965
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17

Search completed: November 8, 2002, 19:29:44 Job time : 12.0654 secs

ö

.; 0

Query Match 5.3%; Score 31; DB 12; Length 1894; Best Local Similarity 19.0%; Pred. No. 3.2e+02; Matches 4; Conservative 0; Mismatches 17; Indels

δŏ

```
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 422, Application US/09833790
| Patent No. US2002066288A1
| Fatent No. US2002066288A1
| GENERAL INFORMATION:
| APPLICANT: Lodge, Michael J.
| APPLICANT: Wang, Tongtong
| APPLICANT: Gerrist, Heather
| APPLICANT: Gerrist, Heather
| APPLICANT: Mohamath, Raodoh
| APPLICANT: Farm, Ligun
| APPLICANT: Farm, Ligun
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION NUMBER: 2001-04-11
| NUMBER OF SEQ ID NOS: 440
| SEQ ID NO 429
| SEQ ID NO 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.3%; Score 31; DB 10; Length 629; Best Local Similarity 50.0%; Pred. No. 1e+02; Matches 6; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                DB 10; Length 559; 92;
                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                Score 31;
Pred. No.
                                                                                                                                                                                                                                          CLONE: 496120
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <URKNOWN>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHRACTERIZICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-052-586-97; Sequence 97, Application US/10052586; Patent No. US20020127584A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              Query Match 5.3%;
Best Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
                                                                                                                                                                                                                        LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney, Austin L
                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                  109 LRTEHXVXXLPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens US-09-833-790-429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 LRTEHXVXXLPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 LRSEESVSRLPE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 : i i i i 1
59 LRVDHSVTSLHD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-833-790-429
                                                                                                                                                                                                                                                                                     US-09-836-561-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
FILE REFERENCE: PAGADIANA THE SAME
CURRENT PAPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 1997-09-18
PRIOR PAPLICATION NUMBER: G0/059263
PRIOR PAPLICATION NUMBER: G0/059266
PRIOR APPLICATION NUMBER: G0/059266
PRIOR APPLICATION NUMBER: G0/059266
PRIOR APPLICATION NUMBER: G0/063120
PRIOR PAPLICATION NUMBER: G0/063120
PRIOR PAPLICATION NUMBER: G0/063120
PRIOR PAPLICATION NUMBER: G0/063121
PRIOR PAPLICATION NUMBER: G0/063121
PRIOR PAPLICATION NUMBER: G0/063121
PRIOR PAPLICATION NUMBER: G0/063340
PRIOR PAPLICATION NUMBER: G0/063540
PRIOR PAPLICATION NUMBER: G0/063541
PRIOR PAPLICATION NUMBER: G0/063131
PRIOR PAPLICATION NUMBER: G0/07320
PRIOR PAPLICATION NUMBER: G0/07321
PRIOR PAPLICATION NUMBER: G0/07323
PRIOR PAPLICATION NUMBER: G0/07323
PRIOR PAPLICATION NUMBER: G0/07333
PRIOR PAPLICATION NUMBER: G0/07333
PRIOR PAPLICATION NUMBER: G0/08333
PRIOR PAPLICATION NUMBER: G0/08333
PRIOR PAPLICATION NUMBER: G0/08333
PRIOR PAPLICATION NUMBER: G0/08333
PRIOR PAPLICATION NUMBER: G0/080333
PRIOR P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081070
FILING DATE: 1998-04-08
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guegler, Karl J.
TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 10; Length 559;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                           APPLICATION OF THE TOTAL OF THE TOTAL OF INVENTION: Human Extracellular Matrix-1 FILE REFERENCE: PF2203C1
CURRENT APPLICATION NUMBER: US/09/854,549
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 09/007,105
PRIOR FILING DATE: 1998-01-14
PRIOR FILING DATE: 1997-01-16
PRIOR FILING DATE: 1997-01-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ć;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <URNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0333 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,561
FILING DATE: 16-Apr-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/212,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            ; Sequence 7, Application US/09854549; Patent No. US20010034334A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 6, Application US/09836561
; Patent No. US20020038006A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.3%;
Best Local Similarity 50.0%;
Matches 6; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
                                                            353 IKSHHNVGGLPD 364
                             109 LRTEHXVXXLPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mus musculus
US-09-854-549-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 LRTEHXVXXLPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-836-561-6
                                                                                                                                                                      US-09-854-549-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEO ID NO 7
                               Qγ
                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.3%; Score 31; DB 10; Length 523;
41.7%; Pred. No. 86;
tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Anamoto, Robert T.
APPLICANT: An H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
84;
                                      FRICK PILLING DATE: 2000-05-23

PRIOR FILLING DATE: 2000-05-23

PRIOR FILLING DATE: 2000-05-26

PRIOR PILLING DATE: 2000-05-26

PRIOR PILLING DATE: 2000-10-23

PRIOR PILLING DATE: 2000-10-23

PRIOR FILLING DATE: 2000-11-27

PRIOR FILLING DATE: 2000-12-22

PRIOR FILLING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: PASTSEQ for Windows Version 4.0

SERIOTH: 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILLE REPERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT PILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10987
LENGTH: 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10987, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
FILING DATE: 2000-03-21 APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Haemophilus influenzae US-09-815-242-10987
                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.3%;
Best Local Similarity 29.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 KXXXXLRTEHXVXXLPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 KTAQTIKSHHNVGGLPE 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-815-242-10987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
    PRIOR
```

δλ q

```
104 KXXXXLRTEHXVXXLPD 120
                                                                                                                                   RESULT 9
US-09-815-242-11555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-815-242-12406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
            οy
                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: Position: 21134..21754 /gene: L3 /product: L3 /order: L3 /broduct: L3 US-09-970-711-13
## APPLICANT: Schaffner, Gotthold
### TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
### FILE REPERENCE: 0652.1800001
### CURRENT APPLICATION UNBER: US/09/970,711
### CURRENT FILING DATE: 2001-10-05
### PRIOR FILING DATE: 1999-01-12
### PRIOR FILING DATE: 1999-01-12
### PRIOR FILING DATE: 1997-04-18
### PRIOR FILING DATE: 1997-04-18
### SOFTWARE: PatentIn Ver. 2.0
### SOFTWARE: PatentIn Ver. 2.0
### ILINGTH: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: 27981nd, JUGILN W.
APPLICANT: 47841nd, JUGILN W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tarwick, John D.
APPLICANT: Tarwick, John D.
APPLICANT: Yamancto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: IDENTIFICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,939
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.3%; Score 31; DB 10; Length 506; 29.4%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 10; Length 206;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5490
LENGTH: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5490, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Staphylococcus aureus US-09-815-242-5490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.3
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.3
Best Local Similarity 29.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 LRRETALNALPENH 205
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: CELO Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-815-242-5490
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qα
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 10; Length 508;
Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ASTILLA.
APPLICANT: ASILD.
APPLICANT: ASILD.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Vu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.O11A
FILE REPERENCE: ELITRA.O11A
FILE REPERENCE: ELITRA.O13-21
PRIOR APPLICATION NUMBER: 60/20/3-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-10-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION:
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                  Sequence 11555, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12406, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRGANISM: Helicobacter pylori
US-09-815-242-11555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
331 KTAQTIKSHHNVGGLPE 347
                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.3
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 IKTHHNVGGLPE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 LRTEHXVXXLPD 120
```

ô

Ş

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 10; Length 40;
Pred. No. 6.2;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N: MAP TO APPO00459.2

N: EXPRESSED IN BF474, SIGNAL = 73

N: EXPRESSED IN BF47L LIVER, SIGNAL = 28

N: EXPRESSED IN HULLO, SIGNAL = 83

N: EXPRESSED IN HERRY, SIGNAL = 19

N: EXPRESSED IN LUNG, SIGNAL = 14

N: EXPRESSED IN BRAIN, SIGNAL = 59

N: EXPRESSED IN PLACENTA, SIGNAL = 7.3

N: EXPRESSED IN PLACENTA, SIGNAL = 54

N: EXPRESSED IN HELA, SIGNAL = 54

N: EXPRESSED IN HELA, SIGNAL = 56

N: EXPRESSED IN HELA, SIGNAL = 56

N: EXPRESSED IN HELA, SIGNAL = 56

N: EXPRESSED IN HELA, SIGNAL = 30

N: EXPRESSED IN HELA, SIGNAL = 30

N: EXPRESSED IN HELA, SIGNAL = 60

N: EXPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IN BONE MARROW, SIGNAL = 30
HIT: BE300193.1, EVALUE 4.00
HIT: Q49412, EVALUE 4.70e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-07
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00665
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-09-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-970-711-13
; Sequence 13, Application US/09970711
; Patent No. US20020081279A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cotten, Matthew
Chiocca, Susanna
Kurzbauer, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baker, Adam APPLICANT: Cotten, Mat APPLICANT: Chiocca, Su APPLICANT: Kurzbauer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: B
OTHER INFORMATION: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-34686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34686, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXPRESSED IN LUNG, SIGNAL = 1

EXPRESSED IN BRAIN, SIGNAL = 1.2

EXPRESSED IN BONE MARROW, SIGNAL = 1.1

EXPRESSED IN ADULT LIVER, SIGNAL = 0.9

EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

EST_HUMAN HIT: BF529379.1, EVALUE 3.00e-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.3%; Score 31; DB 10; Length 30; 42.9%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                          PRIOR PILICATION NUMBER: GB 2423.0
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION WHERE: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (| :| | | | LRPKHLAQPLPPAH 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-864-761-34686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-864-761-42872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
```

ŏ pp ó

```
Sequence 42872, Application US/09864761
Sequence 12872, Application US/09864761
Patent No. US2002004876341
GENERAL INCORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CHER FEFERENCE: Acomica-X-1
CHER TAPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09946143
Patent No. US20020048795A1
GENERAL INFORMATION:
APPLICANT: FARMICK, Mike
TITLE OF INVENTION:
FILE REFERENCE: 032301 WD 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: MAP TO AL118499.5

CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96

CTHER INFORMATION: EST_HUMAN HIT: BE278123.1, EVALUE 1.00e-20

US-09-864-761-46893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%; Score 32; DB 10; Length 337; 62.5%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches 14; Indels
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46893
LENGTH: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.4%; Score 32; DB 10;
Best Local Similarity 28.0%; Pred. No. 5.1;
Matches 7; Conservative 4; Mismatches 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/946,143
CURRENT FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 HXVXXLPDXHXXLXXXDXXXYLLXI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 HVVATMPDLYHLLVELNAVQSLLGL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 YLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 YLLRMWQP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-09-864-761-42872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-946-143-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-946-143-2
                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46893, Application US/09864761
September 10, 0825020044878341
September 10, 0825020044878341
September 10, 0825020044878341
September 10, 082502004487841
September 10, 08250204487841
September 10, 0825020448881
September 10, 082502044881
September 10, 082502044881
September 10, 082502044881
September 10, 082502044881
September 10, 08250204481
September 10, 082502044881
September 10, 08250204481
September 10, 082502040481
September 10, 08250204041
September 10, 
                         APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REPERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT PILLING DATE: 2002-03-27
PRIOR FILLING DATE: 2001-01-16
PRIOR FILLING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PATENTIN VIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 33.3%; Score 37; DB 9; Length 3503; Best Local Similarity 33.3%; Pred. No. 29; Mismatches 7; Conservative 2; Mismatcher 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 DXHXXLXXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 DGHFALTTRDNSIYLVIVHLP 408
      Bachmann, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-864-761-46893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-108-605-237
                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 237
LENGTH: 3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | || : ||: |
42 ROEHFIKGLPEYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-764-855-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46893, p. Sequence 2, Appli Sequence 34866, A Sequence 34686, A Sequence 11555, A Sequence 11555, A Sequence 11555, A Sequence 7, Appli Sequence 6, Appli Sequence 97, Appli Sequence 97, Appli Sequence 97, Appli Sequence 16, Appli Sequence 11, Appli Sequence 51, Appli Sequence 33578, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 121, App
                                                                                      8, 2002, 19:26:04; Search time 9.06536 Seconds (without alignments) 464.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                               Sequence 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gnz_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/prodata/1/pubpaa/DCT02_NEW_PUB.pep:*
/cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US00_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-864 761-46893
US-09-946-143-2
US-09-946-143-2
US-09-946-143-2
US-09-970-711-13
US-09-970-711-13
US-09-815-242-1406
US-09-815-242-11555
US-09-815-242-110987
US-09-815-242-10987
US-09-815-242-10987
US-09-813-561-6
US-09-83-561-6
US-09-83-561-6
US-09-933-777-16
US-09-777-16
US-09-903-456-41
US-09-903-456-41
US-09-903-456-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-764-855-121
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          92612 seqs, 14418503 residues
                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           protein search, using sw model
                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
                                                                                        November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sed
                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB :
                                                           OM protein
                                                                                                                                                                                   Sednence:
                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽.
```

```
Sequence 66, Appl
Sequence 12, Appl
Sequence 85, Appl
Sequence 1261, Appl
Sequence 1261, Appl
Sequence 1261, Appl
Sequence 1261, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 101, Appl
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 103,
                                  Sequence
0. 0S-09-864-761-33661

0. 0S-09-164-864-800

0. 0S-09-111-284-229

2. 0S-10-078-929-66

0. 0S-09-912-020-350

0. 0S-09-913-12

0. 0S-09-913-456-85

0. 0S-09-903-456-65

0. 0S-09-903-456-65

0. 0S-09-903-456-65

0. 0S-09-903-456-65

0. 0S-09-903-486-1261

0. 0S-09-903-866-55

0. 0S-09-903-888-2

0. 0S-09-806-888-2

0. 0S-09-806-808-31
                                                                                                                                                                                                                                                                                                                         US-09-864-761-49072
US-09-894-018-97
US-09-894-018-101
US-09-894-018-95
US-09-894-018-93
US-09-894-018-103
   000000
                                                                                                                                                                                                                                                             10
10
10
9
 199
209
210
214
234
283
292
292
292
423
502
1427
1497
4440
4740
272

      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
```

```
. LOCATION: (231)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-855-121
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
COGATION: (152)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Section 12. Solution US/09764855

Patent No. US20020119919A1

GENERAL INFORMATION:

APPLICANT: ROSen et al.

TITLE OF INVENTION:

FILE REFERENCE: PA110

CURRENT FILIO DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 334

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 121

LENGTH: 233
                                                                                                                                                                                   or file wrapper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 10;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-108-605-237
Sequence 237, Application US/10108605
Patent No. US20020160934A1
GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 RTEHXVXXLPDXH 122
```

THIS PAGE BLANK (USPTO)

```
RESULT 15
F81423
L-lactate permease Cj0076c [imported] - Campylobacter jejuni (strain NCTC 11168)
C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C; Accession: F81423
R; Parkhill, J; Wren, B.W; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A; Tille: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A; Tille: The genome sequence of the food-borne pathogen
A; Reference number: A81250; MUID:20150912; PMID:10688204
A; Accession: F81423
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-560 - PARA
A; Residues: 1-560 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.9%; Score 35; DB 2; Length 560; Best Local Similarity 25.0%; Pred. No. 35; Matches 8; Conservative 2; Mismatches 22; Indels
                                                                     18; Indels
Best Local Similarity 26.7%; Pred. No. 26;
Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                       111 TEHXVXXLPDXHXXLXXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                                  260 TOGOMVNVNDSLVQLTPSDNPYYCLVLWVP 289
                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                           QQ
```

Qy Dp Search completed: November 8, 2002, 19:26:48 Job time: 24.085 secs

9 13:04:27 2002

Sat Nov

```
F;156-172/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.9%; Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 LKKNHSVRAMPAVHSLLNDCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                       109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                 358 LNSDHFTSSMPDLH 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-411 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: AB0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: YP00099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adjustment and makes; protein NOTS; protein YNL267w

Nilternate names; protein NOTS; protein YNL267w

C.Species: Saccharomyces cerevisiae

C.Species: Saccharomyces

C.Species: Saccharomyces

C.Species: Saccharomyces

R.Scharce 262, 144-1448

R.Scharce 262, 144-1448, 1993

R.Scharce 262, 144-1448, 1993

R.Scharce 262, 144-1448, 1993

A.Status: nucleic acid sequence not shown

A.Molecule type: DNA

A.Residues: 11066 A.R.A

A.Residues: 26-43:152-169;255-267;292-305;332-335;434-452;515-530;543-561;603-609;698-71

R.Scharce 262, 144-1448

A.Molecule type: DNA

A.Residues: 26-43:152-169;255-267;292-305;332-335;434-452;515-530;543-561;603-609;698-71

R.Scharce 262, 144-1448

A.Molecule type: DNA

A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-106 (SEW)
A; Residues: 1-106 (SEW)
A; Cross-references: BMBL:271543; NID:g1302325; PIDN:CAA96174.1; PID:e239719; PID:g130232
A; Experimental source: strain $288C
B; Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
Yeast 12, 505-514, 1996
A; Fitle: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sa
A; Reference number: $65111; MUID:96310631; PMID:8740425
                   A;Cross-references: GB:AE004723; GB:AE004091; NID:g9949067; PIDN:AAG06364.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
                                                                                                                                                                                                                                                                                                                                            ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63231.1; PID:g1045243 R;Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H. submitted to the Protein Sequence Database, April 1996 A;Reference number: S63235 A;Reference number: S63235 A;Accession: S63240
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                          Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: SGD:S0005211; MIPS:YNL267w
A;Map position: 14L
C:Keywords: nucleus; phosphotransferase; transmembrane protein
                                                                                                                                                                                                                                                              Score 36; DB 2;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 721-960 <SEF>
                                                                                                                                                                                                                                                              6.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SGD: PIK1; PIK41; PIK120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: X92494
                                                                                                                                        A;Gene: rne; PA2976
C;Superfamily: ribonuclease E
                                                                                                                                                                                                                                                                                                                                                                                                           109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 LRTRARIFILPDDH 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-1066 <SEN>
A; Residues: 1-1057 <STO>
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
C; Accession: D69786
R; Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Ber C; Bron, S; Brouillet, S; Bruschi, C.V; Caldwall, B; Capuano, V; Carter, N.M; A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fabret, C; Ferrari, Nature 390, 249-256, 1997
A; Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Galicch, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S; Hosono, S; Hullo, M Koetter, P; Koningstein, G; Krogh, S; Kumano, M; Kurita, R.; Lapidus, A; Lardino, A; Authors: Lauber, J; Lazarevic, V; Lee, S.M; Levine, A; Liu, H; Masuda, S; Mau Y, M; Ogawa, K; Ogiwara, A; Oudeqa, B; Park, S.H; Parro, V; Pohl, T.M; Portete Rieger, M; Rivolta, C; Rocha, B; Roche, B; Rose, M; Sadie, Y; Sato, T; Scanla, Authors: Schleich, A; Tanakoshi, A; Tanaka, T; Terpstra, P; Tognoni, A; Tosato, V; Uchiya T; Winters, P; Wipat, A; Yamanoto, H; Yamane, K; Yasamoto, K; Yata, K; Yoshida A; Authors: Yoshikawa, H; Danchin, A; Tosato, V; Uchiya A; Title: The complete genome sequence of the Gram-Positive bacterium Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: ABB001: W.) Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G dil, M.; Ruhberford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Accession: D69786
A.Status: preliminary: nucleic acid sequence not shown; translation not shown A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-229 <a href="https://doi.org/10.10/">KCMNA
A.Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12411.1; PID:g26329
                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AL590842; PIDN: CAC88964.1; PID: 915978208; GSPDB: GN00175 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable exported protein YPO0099 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                              919/coprotein endopeptidase homolog ydic - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                       ;
0
Length 1066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 229,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
16;
Score 36; DB 2;
Pred. No. 37;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain 168
C; Genetics:
A; Gene: ydiC
C; Superfamily: hypothetical protein H10388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 LRTEHXVXXLPDXHXXLXXXD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.98;
33.38;
   6.18;
|larity 35.78;
|Conservative
```

DB 2; Length 411;

```
110 RTEHXVXXLPDXHXXLXXXD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 DXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 DTAVYLANIWTP 152
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: STY3033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
H83273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pp
                                                                                                                                                                                                                                                                                                                                                                                         oscillatory nuclear movement
                                                                                                                                                                                                   RESULT 7
T43774
dynein heavy chain, cytosolic - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C; Accession: T43274
B; Yamamoto, A: West, R.R.; McIntosh, J.R.; Hiraoka, Y.
J. Cell Biol. 145, 1233-1250, 1999
A; Title: A cytoplasmic dynein heavy chain Is required for oscillatory nuclear movem A; Reference number: 222383; MuID:99296615; PMID:10366596
A; Accession: T43274
A; Residues: 1-4196 < YAM>
A; Reperimental source: strain CRLi52
A; Genetics:
A; Genetics:
A; Genetics:
A; Ganetics:
A; Gaperfamily: dynein heavy chain, cytosolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ayorthetical protein W04D2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Accession: T26148
R;Lennard, N.
Submitted to the EMBL Data Library, June 1996
A;Reference number: 220161
A;Accession: T26148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T26148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross references: EMBL:275552; PIDN:CAA99942.1; GSPDB:GN00023; CESP:W04D2.4
A;Experimental source: clone W04D2
C;Genetics:
A;Gene: CESP:W04D2.4
A;Map position: 5
A;Introns: 23/3; 112/3; 183/2; 402/2; 495/1; 523/3
                                                     ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:CAA99942.1; GSPDB:GN00023; CESP:W04D2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  succinoglycan biosynthesis regulator (exsB) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2,
DB 2; Length 1540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 4196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 624;
                                                     13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 45;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.3%; Score 37; DB 64.3%; Pred. No. 14; ive 0; Mismatches
         Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38;
                                                                                                                                    990 DHDVSTLHDLHNALRGVDNVLY 1011
                                                                                               112 EHXVXXLPDXHXXLXXXDXXXY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1140 SEHLLNELDDTHSSLSTVD 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.4%;
Best Local Similarity 36.8%;
Matches 7; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 TEHXVXXLPDXHXXLXXXD 129
         6.48;
    Query Match
Best Local Similarity 36.43
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.3
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRIEHDV--LPDVH 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
B69305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                 δ
                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
```

```
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999 C;Accession: B69305
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod.; Felischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E Glodek, A.; Zhou, L.; Quackenbush, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A;Reference number: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Salmonella enterica subsp. enterica servar Typhi
A;Note: this species has also been called Salmonella typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C; Accession: AH0853
B; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L.; White, N.; Farr
S; Moule, S; O'Gaora, P.
Nature 413, 848-852, 2001
A; Reference number: AB0502; PMID:11677608
A; Reference number: AB0502; PMID:11677608
A; Accession: AH0853
A; Accession: AH0853
A; Accession: AH0853
A; Accession: AH0853
A; Accession: Anosa A; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-239 <KLE>
A;Cross-references: GB:AE001074; GB:AE000782; NID:92689397; PIDN:AAB90792.1; PID:9265
C;Superfamily: conserved hypothetical protein HI1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              АНО853
DNA mismatch repair protein [imported] - Salmonella enterica subsp. enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.; Hickey,
A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-855 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06015.1; PID:g16503984; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tibonuclease E PA2976 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: H83273 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%; Score 36; DB 2; 35.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2
Pred. No. 9.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: DNA mismatch repair protein mutS
```

N

ö

Gaps

; 0

```
polyfulus Synthase Important in Synthesis in Synthase Important in Synthase Impor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Gene: pksc
C; Superfamily: Streptomyces hygroscopicus probable polyketide synthase module 4; 3-ox
homology; [acyl-carrier-protein] S-malonyltransferase homology
C; Keywords: carrier protein
F;54-455/Domain: 3-oxoacyl-(acyl-carrier-protein] synthase I homology <OAS2>
F;563-840/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1155-1334/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: ML2356
C;Superfamily: Streptomyces hygroscopicus probable polyketide synthase module 4; 3-ox
homology; [acyl-carrier-protein] S-malonyltransferase homology
C;Reywords: carrier protein
                                  A,Cross-references: FlyBase:FBgn0014075
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F;1-22/Domain: signal sequence #status predicted <SIG>
F;1-23/Domain: signal sequence #status predicted in glucosyltransferase #status experimental
F;181,266,864/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyketide synthase pksC - Mycobacterium leprae
Nalternate names: L518_F1_2 protein
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S73013
R;Smith, D.R; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid L518.
A;Reference number: S72591
A;Reference number: S72591
A;Accession: S73013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1446 <SMI>A;Cross_references: EMBL:U00023; NID:q467194; PIDN:AAA17356.1; PID:q467199
                                                                                                                                                                                                                                                                                 Query Match 6.9%; Score 41; DB 2; Length 1548; Best Local Similarity 28.2%; Pred. No. 3.9; Matches 11; Conservative 2; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 38; DB 2; Length 1446; 36.4%; Pred. No. 17; tive 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyketide synthase [imported] - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 PXXXXXXXXXXXXLRTEHXVXXLPDXHXXLXXXXXXXYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           935 РКОТКТКЕК ГРТОГКТОН SVVK ГРРКОЕК ГРНЕ БУВАР 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990 DHDVSTLHDLHNALRGVDNVLY 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 EHXVXXLPDXHXXLXXXDXXXY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
            A; Gene: FlyBase: Ugt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 4
A;Introns: 41/3; 70/3; 88/1; 118/1; 321/1; 367/1; 474/1; 504/2; 624/3; 655/2; 667/3; 695
A;Note: F28A23.180
C;Superfamily: Arabidopsis thaliana hypothetical protein F28A23.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Drosophila melanogaster
C;Date: 23-Aug-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: S54723; S54724
R;Parker, C.G.; Fessler, L.I.; Nelson, R.E.; Fessler, J.H.
EMBO J. 14, 1294-1303, 1995
A;Title: Drosophila UDP-glucose:glycoprotein glucosyltransferase: sequence and character
A;Reference number: S54723; MUID:95246722; PMID:7729408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UDP-glucose-glycoprotein glucosyltransferase (EC 2.4.1.-) precursor – fruit fly (Drosoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F28A23.180 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: T05430
R; Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; Submitted to the Protein Sequence Database, October 1998
A; Reference number: 215415
A; Accession: T05430
A; Molecule type: DNA
A; Residues: 1-917 < CEEV
A; Residues: 1-917 < CEEV
A; Residues: 1-917 < CEEV
A; Cross-references: EMBL: AL021961
A; Experimental source: cultivar Columbia; BAC clone F28A23
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
•
                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1207 <STO>
A;Cross-references: GB:AE002093; NID:g4581149; PIDN:AAD24633.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1094 KNISQLRTEHRVYELPDEHPLLAQLEKREPDDPCSYLLAIWTP-GETADSIQPSVSTC-- 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: S54723
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1548 <PAR>
A;Cross-references: GB:U20554; NID:g790584; PIDN:AAA85850.1; PID:g790585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 77; DB 2; Length 917;
Pred. No. 2.4e-08;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 KXXXXLRTEHXVXXLPDXHXXL-----XXXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 91; DB 2; Dred. No. 2.3e-11; O; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151 -IFQANGMLCDEETCFSCNSIKETRSQIVRGTIL 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.4%;
29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.1%;
Best Local Similarity 44.2%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.89
Watches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-37 <PA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S54724
                                                                                                                                                                                                                                                                                                                           A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Conetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

ö

Gaps

5.1.3 Compugen Ltd. version - 2002 GenCore Copyright (c) 1993

protein search, using sw model OM protein 8, 2002, 19:24:14; Search time 19.085 Seconds (without alignments) 1470.857 Million cell updates/sec November Run on:

US-09-840-743-73 590 Title: Perfect score:

Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

length: 0 length: 200000000 sed Minimum DB : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		_	_	UDP-glucose-glycop		polyketide synthas	dynein heavy chain	hypothetical prote	succinoglycan bios	DNA mismatch repai	ribonuclease E PA2	1-phosphatidylinos	glycoprotein endop	probable exported	L-lactate permease	ĭ	(1)	probable thioredox	transcription regu	hypothetical prote		ption		monooxygenase homo	GMP synthase (glut	Putative L-lactate	L-lactate permease	probable L-lactate	formate dehydrogen
SUMMARIES	,																													
SUMM	ឧ	T48454	$\sim$	T05430	S54723	S73013	н87203	T43274	T26148	B69305	AH0853	н83273	A49335	D69786	AB0013	F81423	H90451	T10358	B72454	D87450	н81213	B81790	A87451	m	m	703	m	8302	75	1355
	DB	7	7	7	7	(7)	~	~1	7	7	7	7	7	7	7	~	7	7	7	7	~	7	7	7	7	7	7	7	7	7
	Length	234	1207	917	1548	1446	1540	4196	624	239	855	1057	1066	229	411	260	762	249	250	298	322	322	335	459	499	510	260	562	267	786
о¥Р	Query	24.7		3	6.9	6.4	6.4	•	6.3		•		٠	•	•	•			5.8	•	•									
	Score	1	91	77	41	38	38	38	37	36	36	36	36	35	32	32	32	34	34	34	34	34	34	34	34	34	34	34	34	34
	Result No.	н	7	m	4	5	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

general secretion hypothetical prote	hypothetical prote	halocyanin precurs	probable alkyl hyd	probable peroxired	hypothetical prote	RNA polymerase alp	probable transposa	. glycosyl transfera	probable aminometh	hypothetical prote	DNA mismatch repai	thiazide-sensitive	O-antigen biosynth	phosphoinositide 3
D87271 T21490	T21486	G84236	C71065	C75081	T05450	A82715	S16891	G95205	D97532	AD2751	AD0407	A47296	T18556	T13801
77	7	7	7	ď	ď	C	7	7	7	7	7	7	7	7
368 106	142	157	216	216	264	332	380	398	473	473	851	1023	1275	1876
5.7	5.6	9.6	5.6	9.6	5.6	5.6	9.6	9.6	5.6	5.6	5.6	5.6	9.6	5.6
33.5 33	33	33	33	33	33	33	33	33	33	33	33	33	33	33

## ALIGNMENTS

hypothetical protein T32M21.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48454
R:Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; Submitted to the Protein Sequence Database, March 2000
A:Accession: T48454
A:Accession: T48454
A:Sterius: preliminary
A:Molecule type: DNA
A;Residues: 1-234 <BEV>
A;Residues: 1-234 <BEV>
A;Residues: 1-234 <BEV>
C:Genetics: Cultivar Columbia; BAC clone T32M21

A;Map position: 5 A;Introns: 49/2; 61/3; 81/1; 127/3; 149/3; 188/1; 201/1 A;Note: T32M21.180

10; 24.7%; Score 146; DB 2; Length 234; 26.2%; Pred. No. 3e-24; tive 0; Mismatches 134; Indels 1 Conservative Query Match Best Local Similarity Matches 51; Conserv

3;

ŏ g

óγ

95 -GGKASGKMCFDETCSECNSLREANSQTVRGTLLIPCRTAMRGSFPLNGTYFQVNELFAD 153 q

δλ

154 HESSLKPIDVPRDWIWDLPRRTVYFGTSVTSIFRGLSTEQIQFCFWKGFVCVRGFEQKTR 213 g

278 XPXXLXXXLHXXXSK 292 | | | | || || || || 214 APRPLMARLHFPASK 228 ŏ

Dp

RESULT 2 D84781

hypothetical protein At2936490 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: D64781
R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999

THIS PAGE BLANK (USPTO)

```
Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Mon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nania A. Dr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
Nania A. Dr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasai H.E.,
de Soluza A.C.R., da Silve A.M., da Silva F.R., Silva W.A. Jr.,
A da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
A da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
A vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000).
C. P. DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.lsb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RNA)(N) SUBUNIT: CONSISTS OF A SIGMA FACTOR AND THE RNAP CORE ENZYME WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, 1 BETA' CHAIN AND 1 OMEGA CHAIN (BY SIMILARITY).

DOMAIN: THE AMINO-TERMINAL PORTION IS INVOLVED IN THE ASSEMBLY OF CORE RAPA, WHEREAS THE CHEMINAL IS INVOLVED IN INTERACTION WITH TRANSCRIPTIONAL REGULATORS (BY SIMILARITY).

SIMILARITY: BELONGS TO THE RNA POLYMERASE ALPHA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%; Score 33; DB 1; Length 332; 35.7%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR01700; RNA_pol_A_bac.
Pfam: PF01000; RNA_pol_A_bac; 1.
Pfam: PF03118; RNA_pol_A_CTD; 1.
ProDom; PD001179; RNA_pol_A_bac; 1.
Transferase; Transcription; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 332 AA; 36554 MW; 98BDE535F753A577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003951; AAF83986.1; -. HSSP; P00574; 1COO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35./*,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBSTRATES.
                  RRAPA RRAPA
```

Search completed: November 8, 2002, 19:27:16 Job time : 15.4967 secs

;

Gaps

;

5; Indels

4; Mismatches

109 LRTEHXVXXLPDXH 122 ::|:| | : | | 115 IKTDHNVEIINDGH 128

δy g ω

```
NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylella.
NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=9a5c;
                                                                                                                                                                                                                                                                                                                                                                                                                                            RPOA_XYLFA
Q9PE52;
                                                                                                                                                                                                                                                                                                  ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                          g
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                                                                                                                                                                     Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
                                                                         ;;
0
                                                                                                                                                                                                                                                                                                                               structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TDXH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 1; Length 216;
Pred. No. 11;
                                                     Length 142;
                                                                        3; Indels
                               142 AA; 16075 MW; B496362F0BFEC354 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COA5BEE514612179 CRC64;
                                                    Score 33; DB 1;
Pred. No. 7.1;
                                                                                                                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable peroxiredoxin.
                                                                                                                                                                 216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 AA
                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
TIGRFAMS; TIGR01080; rplX_A_E; 1.
PROSITE; PS01108; RIBOSOMAL_L24; 1.
Ribosomal protein.
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ248286; CAB49952.1; -. HSSP; P30041; 1PRX.
InterPro: IPR000866; AhpC-TSA.
Pfam; PF00578; AhpC-TSA; 1.
Antioxidant; Complete proteome.
ACT_SITE 46 BY SEQUENCE 216 AA; 24758 MW; CO
                                                     5.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.6%;
                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                 Probable peroxiredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 LRTEHXVXXLPD 120
                                                                                           109 LRTEHXVXXLP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 VKTTHGVIKLPD 24
                                                                                                       |||:| : :|
38 LRTKHGIRAIP 48
                                                                                                                                                                                                                                                                                                 STRAIN-GE5 / Orsay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Pyrococcus abyssi.
                                                                                                                                                                                                                                                                  NCBI_TaxID=29292;
                                                                                                                                                                                   16-OCT-2001
                                                                                                                                                                                             16-OCT-2001
16-OCT-2001
                                                                                                                                                                TDXH_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDXH_PYRHO
058966;
                                                                                                                                                                                                                                                                                                            Heilig R.;
                                SEQUENCE
                                                     Query Match
                                                                                                                                                                           Q9UZV4;
                                                                                                                                                                                                                           PAB1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PH1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDXH_PYRHO
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE DE DE OCC SCOOL
                                                                                                                                                                          DR DR
                                                                                           ò
                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
A Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
A Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brinnes M.R.S.,
Bueno M.R.P., Camargo A.A., Canargo L.E.A., Carraro D.M., Carrer H.A.
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias.Neto E., Docena C., El-Dorry H.,
A Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
A Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Ganier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
A Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitalima J.P.,
Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Lemos E.G.M., Lemos M.V.F., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
                                  Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takaniya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; "Complete sequence and gene organization of the genome of a hyper-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-027-2001 (Rel. 40, Created)
16-027-2001 (Rel. 40, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (Transcriptase alpha chain) (RNA polymerase alpha subunit).

RPOA OR XF1176.
Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                   thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
-!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TDXH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.6%; Score 33; DB 1; Length 216; 50.0%; Pred. No. 11; 4; Indels iive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
A95DF14BF3874CA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20365717; PubMed-10910347;
MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P30041; IPRX.
InterPro; IPR000866; AhpC-TSA.
Pfam; PF00578; AhpC-TSA: 1.
Antioxidant; Complete proteome.
ACT_SITE 46 46 B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP000005; BAA30317.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 AA; 24757 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 LRTEHXVXXLPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 VKTTHGVIKLPD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
```

```
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2300
                                                                                                                                                                                                                                                                1056
1081
1122
11143
11143
11189
1213
1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1513
1564
1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1422
                                                 Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RL26_CAEEL
Q19869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
                                                   yase;
                                                                                                REPEAT
REPEAT
                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                            REPEAT
                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
RL26_CAEEL
                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
    SO SETT THE FETT THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92000795; PubMed=1680356;
Kore-Eda S., Murayama T., Uno I.;
"Isolation and characterization of the adenylate cyclase structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
1-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene of Neurospora crassa.";
Jpn. J. Genet. 66:317-334(1991).
-!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.-:- SIMILARITY: BELONGS TO ADBNIVIL OTCLASE CLASS-3 FAMILY.-:- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).-:- SIMILARITY: CONTAINS 1 PP2C-LIKE DOMAIN.
                                                                                                                                                                                                                                                                Score 34; DB 1; Length 560;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                               15; Indels
                                                                                                                                                                                                                 8ECB9F9626FFC40A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 2300 AA.
                                                                                                                                                                                                                                                                                                               1; Mismatches
                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                    POTENTIAL. POTENTIAL.
                                                                                                                                                                   POTENTIAL. POTENTIAL.
  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001054; G_Cyclase.
InterPro; IPR001054; G_Cyclase.
InterPro; IPR001561; LRR.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
InterPro; IPR001932; PP2C-11ke.
InterPro; IPR001932; PP2C-11ke.
InterPro; IPR001959; RA_domain.
Pfam; PF00211; guanylate_cyc; I.
Pfam; PF00560; LRR; I4.
Pfam; PF00560; LRR; I4.
Pfam; PF000660; LEURR; I4.
SMART; SM00044; CYCC; I.
SMART; SM00049; LEURR; CYC; I.
SMART; SM00310; LRR; IRR; I.
SMART; SM00310; LRR; IRR; I.
                                                                                                                                                                                                                                                                                                                                                            118 LPDXHXXLXXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                         58920 MW;
                                                                                                                                                                                                                                                                5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D00909; BAA00755.1; -
                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 30.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
  179
2220
2269
3334
430
558
159
200
226
249
314
379
410
440
538
538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYAA_NEUCR
Q01631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR-1 OR NAC.
                                                                                                                 TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                                                     TRANSMEM
TRANSMEM
  TRANSMEM
TRANSMEM
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAMP
                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyclase)
  ò
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HE STANDARY SECOND STANDARY SECOND SE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burton J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                     CYCLASES_2; 1.
repeat; cAMP synthesis; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 1; Length 2300; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52E79B90E6B17A7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-Sos ribosomal protein L26.
RPL-26 OR F28G6.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        LRR 23.
PP2C-LIKE.
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-SER
                                                                  LRR
LRR
LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 268315; CAA92674.1; -. WormPep; F28C6.7; CE03278. InterPro; IPR000302; KOW_motif. Pfam; PF00467; KOW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.8%;
SMART; SM00314; RA; 1.
PROSITE; PS50125; GUANYLATE_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 KTSSSARSGHSIVHLPGHH 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 KXXXXLRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254752
                                    Leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Query Match
Best Local Similarity 31.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                  914
938
961
961
1008
1031
1079
11079
11120
1142
11188
                                                                                                                                                                                                                                                                                                                                                           1445
1469
1497
1538
1829
2300
221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
```

```
| ::| | ||:
335 KGSAKIKTHHNVGGLPE 351
                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine + H(2)O = AMP + diphosphate + GMP + L-glutamate.
-i- PATHWAY: GMP blosynthesis.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SUBUNIT: IN THE C-TERMINAL SECTION; BELONGS TO THE GMP SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                          Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                         Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6MP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) (Glutamine amidotransferase) (GMP synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00117; GATASS; 1.
PRIME, PF00117; GATASS; 1.
PRIMES; PR00097; ANTSNHASEII.
PRINTS; PR00096; GATASE.
TIGRRAMS; TIGR00884; guaA_Cterm; 1.
TIGRFAMS; TIGR00884; guaA_Nterm; 1.
PROSITE; PS0044; GATASE_TYPE_I; 1.
Ligase; GMP blosynthesis; Purine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLÜTAMINE AMIDOTRANSFERASE.
GMP-BINDING (BR SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 510;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glutamine amidotransferase; Complete proteome.
                                                                                                                     510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002385; Anth_synthII.
InterPro; IPR000991; GATase_1.
InterPro; IPR001674; GMP_synt_C.
InterPro; IPR004739; GMPsynthase_N.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98196666; PubMed-9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000679; AAC06558.1; -. HSSP; P04079; 1GPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57858 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392:353-358(1998)
                                                                                                                     STANDARD;
                       224 TEHSVGFVPD 233
111 TEHXVXXLPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=63363;
                                                                                                                                                                                                                                                            Aquifex aeolicus
                                                                                                                                                                                                                                          GUAA OR AQ_236.
                                                                                                                                                30-MAY-2000
30-MAY-2000
15-JUN-2002
                                                                                                                   GUAA_AQUAE
O66601;
                                                                                                                                                                                                                                                                                                                                                              STRAIN-VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                            Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                     õ
                                 a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-Z11/8909; Pubmed=11283302; MEDLINE-Z11/8909; Pubmed=11283302; Nunez M.F., Pellicer M.T., Badia J., Aguilar J., Baldoma L.; Nunez M.F., Pellicer M.T., Badia J., Aguilar J., Baldoma L.; pellicer M.T., Esdia J., Aguilar J., Baldoma L.; permease for glycolate that is structurally and functionally similar to L-lactate permease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chlorophenylhydrazone (CCCP).
                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                              Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., May B., Shao Y.;
                                                                                                   Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Probable).
-!- INDUCTION: By glycolate.
-!- SIMILARITY: BELONGS TO THE LACTATE PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           motive force.
ENZYME REGULATION: Inhibited by carbonyl cyanide
                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003804; Lactate_perm.
Pfam; PF02652; Lactate_perm; 1
TIGRPAMs; TIGR00795; lctP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             Microbiology 147:1069-1077(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000380; AAC76011.1; -. EcoGene; EG12995; qlcA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U28377; AAA69142.1;
 STANDARD;
                                                                        Glycolate permease glcA. GLCA OR B2975.
                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION
                                                                                                                                                NCBI_TaxID=562;
GLCA_ECOLI
Q46839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
```

;

Gaps

.

8; Indels

3; Mismatches

Conservative

Matches

104 KXXXXLRTEHXVXXLPD 120

Ş

Length 250;

S

```
Query Match
Best Local Similarity
                                                                                                                                                                                                                                   MURF_TREPA
                                               Matches
                                                                                                                                                                                                         RESULT 8
                                                                                                                                    g
                                                                                                                                                                                                                                                        δ
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLIKE-99310339; PubMed-10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagal Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TDXH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 34; DB 1; Length 249; 50.0%; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
; 0457F2852D051E7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             03B17D50DBA9EE4B CRC64;
  SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable peroxiredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                            InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antioxidant; Complete proteome. ACT_SITE 50 50 BY SEQUENCE 250 AA; 28703 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP000064; BAA81290.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000866; AhpC-TSA.
                                                                                                                                                                                                                                                                                                                                                                                          66
28295 MW;
                                                                                                                                                                                                                              EMBL; U75930; AAC59088.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00578; Ahpc-TSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 50.0 nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 LRAERAVKALADAH 206
                                                                                                                                                                                                                                                                                                                                                                                                             249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P30041; 1PRX
                                                                                                                                                                                                                                                                                                                                                                                        æ
                                                                                                                                                                                                                                                                                                                                                                Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDXH_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K1;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                        ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
TDXH_ARERPE
TDXH_ARERPE
TDXH_ARERPE
TD 16-OCT-
DT 16-OCT-
DT 16-OCT-
DT 16-OCT-
DY 16-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
UDP-N-acctylumtramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl liqase (EC 6.3.2.15) (UDP-MurNAc-pentapeptide synthetase)
(D-alanyl-D-alanine-adding enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamyl-meso-2.6-diaminoheptanediodte + D-alanyl-D-alanine - ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-6-carboxy-L-1ysyl-D-alanyl-0-alanine.
-!- PATHWAY: Peptidoglycan blosynthesis.
-!- PATHWAY: Peptidoglycan blosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCIENCE 281:375-388(1998).

-1- FUNCTION: INVOLVED IN CELL WALL FORMATION. CATALYSES THE FINAL STEP IN THE SYNTHESIS OF UDP-N-ACETYLMURAMOYL-PENTAPEPTIDE, THE PRECURSOR OF MUREIN (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
                                                                .
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TICKEAMS; TICKUIL43; murr; I.
Peptidoglycan synthesis; Cell division; Cell wall; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 459;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL).
23EA5571ED95F332 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spirochaetales; Spirochaetaceae; Treponema.
Score 34; DB 1;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%; Score 34; DB 1;
60.0%; Pred. No. 14;
Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                   459 AA
                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR000713; Mur_ligase.
Interpro; IPR004101; Mur_ligase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
TIGRFAMS; TIGR01143; murF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001217; AAC65370.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50234 MW;
5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                          111 TEHXVXXLPDXH 122
                                                                                                                                                                                        19 TDHGVIKLPDHY 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P11880; 1GG4.
TIGR; TP0386; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MURF OR TP0386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                MURF_TREPA
083401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
SEQUENCE
```

4

```
Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCG3_NPVOP
010339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VCG3_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                             ##BL, #BDUDEL.

##BL, #AE00EL.

##BL, #AE07276; CAL.

##BL, #A2868.

##BL, #A2868.

##BR, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia-Bustos J.F., Marini F., Stevenson I., Frei C., Hall M.N.;
"PIKI, an essential phosphatidylinositol 4-kinase associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lanagan C.A., Schnieders E.A., Emerick A.W., Kunisawa R., Admon A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thorner J., "Phosphatidylinositol 4-kinase: gene structure and requirement for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                       FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
Phosphatidylinositol 4-kinase PIK1 (EC 2.7.1.67) (PI4-kinase)
                                         t
step. This protein has a weak ATPase activity.
SIMILARITY: BELDONGS TO THE DNA MISMATCH REPAIR WUTS
CAUTION: Ref.1 sequence differs from that shown due frameshifts in positions 353, 379, 394, 422 and 425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1066 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                               EMBL, U16303; AAA80578.1; ALT_FRAME.
EMBL, M18965; AAAZ1767.1; ALT_FRAME.
EMBL, AE008832; AAL21789.1; -.
EMBL, AL627276; CAD06015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=94069320; Pubmed-8248783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94252322; Pubmed-8194527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 RTEHXVXXLPDXHXXLXXXD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 RMRHAFQQLPELHAQLETVD 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yeast cell viability.";
Science 262:1444-1448(1993).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yeast nucleus.";
EMBO J. 13:2352-2361(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Ptdins-4-kinase).
PIKI OR YNL267W OR N0795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=JK9-3D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIK1_YEAST
P39104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
PIK1_YEAST
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                      Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; The sequence of a 24,152 bp segment from the left arm of chromosome XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.; Funk C.J., Evans J., Harwood S., The harmon G.F.; Funk C.J., Evans J., Harwood S., The orgying pseudotsugata multinucleocapsid nuclear Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                              THE STATE OF THE PRODUCTION OF THE SECOND MESSENGER COMMITTED STEP IN THE PRODUCTION OF THE SECOND MESSENGER INOSITOL, 1, 4, 5, -7 TRISPHOSPHATE, PIKI IS PART OF A NUCLEAR PHOSPHOINOSTIDE CYCLE AND COULD CONTROL CYTOKINESIS THROUGH THE ACTIN CYTOSKELETON.

-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP 1-phosphatidyl-1D-myo-inositol 4-phosphate.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orgyla pseudotsugata multicapsid polyhedrosis virus (OpMNPV). Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X76058; CAA53658.1; -.

R EMBL; L20220; AAA34873.1; -.

R EMBL; X2494; CAA6323.1; -.

R EMBL; X7435; AQA9317.1; -.

R PIR; A4456; S44456.

SGD; S0005211; PIKI.

R Interpro, IPR004043; PI3_PI4_Kinase.

R PROSITE; PS00916; PI3_AKINASE.1; -.

R PROSITE; PS00916; PI3_4 KINASE.1; I.

R PROSITE; PS00916; PI3_4 KINASE.2; I.

R PROSITE; PS00916; PI3_4 KINASE.3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1; Length 1066; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
SEQUENCE FROM N.A.
STRAIN-S288c / FY1679;
MEDLINE-96310631; Pubmed-8740425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=97271300; Pubmed=9126251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 35.7
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein CG30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 LNSDHFTSSMPDLH 371
                                                                                                                                                                                                                            genes.";
Yeast 12:505-514(1996).
```

ö

3

```
110 RTEHXVXXLPDXH 122
                                        41
                                                                                                                      MUTS_SALTY
    δ
                                        g
                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
THE C-TERMINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS50215; ADAM_MEPRO; 1.
PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSITE: PS00427; TSP1, 2.
PROSITE: PS00142; AINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07F9F48E63BD83A3 CRC64;
                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC (CATALYTIC)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWITCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
BY SIMILARITY.
ADAMTS-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
SPACER 2.
TSP TYPE-1 5.
TSP TYPE-1 6.
TSP TYPE-1 7.
TSP TYPE-1 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE-1 1.
                                                                                                                                                                                                                                                                                                                             InterPro; IPR001762; Disintegrin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR000894; TSP1.
InterPro; IPR000180; Zn_MTpeptdse.
Pfan; PP00090; tsp.1; 6.
Pfan; PF01421; Reprolysin; 1.
Pfan; PF01421; Reprolysin; 1.
Pfan; PF01562; Pep_M12B_propep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (N-LINKED (N-LINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPACER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177545 MW;
                                                                                                                                                                                                                                                                        EMBL; AJ250725; CAC20419.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Extracellular matrix.
SIGNAL 1 25
                                                                                                                                                                                                                                                                                             HGNC:14605; ADAMTS12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              951
1104
1275
1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402
105
125
215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
                                                                                                                                                                                                                                                                                                               606184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
```

```
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Daviss R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                              SPECIES-S.typhimurium;
MEDLINE-88086868; PubMed=3275609;
Haber L.T., Pang P.P., Sobell D.I., Mankovich J.A., Walker G.C.;
"Nucleotide sequence of the Salmonella typhimurium muts gene required
for mismatch repair: homology of Muts and HexA of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Detecting frame shifts by amino acid sequence comparison.";
J. 601. Biol. 234:1140-1157(1993).
-!- FUNCTION: This protein is involved in the repair of mismatches in
DNA. It is possible that it carries out the mismatch recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haber L.T., Walker G.C.;
"Altering the conserved nucleotide binding motif in the Salmonella typhimurium MutS mismatch repair protein affects both its ATPase and mismatch binding activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                            Salmonella typhimurium, and
Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION OF PROBABLE FRAMESHIFT IN 394-425
                                                                                                                                                                     (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                               855 AA
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 1-5
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-S.typhi; STRAIN-CT18;
MEDLINE-21534947; PubMed-11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.typhimurium;
MEDLINE=91330898; PubMed=1651234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.typhimurium;
MEDLINE=94087727; PubMed=7903399;
                                                                                                                                                                                                        DNA mismatch repair protein muts MUTS OR STM2909 OR STY3033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eumoniae.";
Bacteriol. 170:197-202(1988)
                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGENESIS, AND ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 10:2707-2715(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
                                                                                                             STANDARD;
| || : ||: |
RQEHFIKGLPEYH 53
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claverie J.-M.;
                                                                                                                                                                   15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                        Salmonella.
                                                                                                           MUTS_SALTY
P10339;
```

ö

Gaps

ö

Indels

Score 37; DB 1; Length 1593;

6.3%; 46.28;

Pred. No. 11;

Conservative

Best Local Similarity Matches 6; Conserv

Query Match

~

INTERMEDIATE AND LIGHT CHAINS

```
οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
 A Squros J. Peat N., Hayles J., Baker S., Basham D., Bowman S.,
    Racolner J. Peat N., Hayles J., Baker S., Basham D., Bowman S.,
    Benoks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
    Benoks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
    Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
    Gentles S., Goble A., Hamiln N., Harris D., Hidalgo J., Hodgson G.,
    Halroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
    A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
    RA Money P., Woule S., Mungall K., Murphy L., Niblett D., Odell C.,
    RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
    Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
    Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
    RA Gabel C., Fuchs M., Squares S., Stevens K.,
    Raylor K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
    Ber P., Zlmmermann W., Wedler H., Wambutt R., Purnelle B.,
    RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
    Ra Loas M., Rochet M., Garzon A., Thode G.,
    RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Garzon A., Thode G.,
    RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Garzon A., Thode G.,
    RA Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
    RA Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
    RA Harte 41:871-880(2002)
                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND ORGANELLES ALONG MICROTUBULES. REQUIRED FOR NUCLEAR MOVEMENT
                                                                                                                                                             Gaps
                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
PREVENT SECRETION FROM ER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                             ;
0
                                                                                                                                  Score 41; DB 1; Length 1548;
                                                                                                       95D6849961622DB6 CRC64;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto A., West R.R., McIntosh J.R., Hiraoka Y.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                          UDP-GLUCOSE:GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                  Dynein heavy chain, cytosolic (DYHC).
DHC1 OR SPAC30C2.01C OR SPAC1093.06C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetae;
                                      GLUCOSYLTRANSFERASE.
                                                                                                                                                                                                                973
                                                                                                                                                                                     96 PXXXXXXXXXXXXXRFHXVXXLPDXHXXLXXXXXXXXI 134
                                                                                                                                                                                                                                                                                DYHC_SCHPO STANDARD; PRT; 4196 AA. 013290; Q996L0; Q9UTPB; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                  Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21848401; PubMed-11859360;
                                                                                                          Ψ.,
                                                                                                                                  6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DURING MEIOTIC PROPHASE.
                                                                                                       1548 AA; 174465
                                                                                                                                                             11; Conservative
                                                 181
266
864
1548
                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                 181
266
864
            1
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CRL152;
Glycoprotein.
                                                               CARBOHYD
CARBOHYD
                                                   CARBOHYD
                                                                                                       SEQUENCE
                                                                                                                                  Query Match
            SIGNAL
                         CHAIN
                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                     DYHC_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>;</u>
                                                                                                                                                                                                                                                        RESULT 2
                                                                                                                                                                                                                                                                                              X T T T T T T T S
                                                                                                                                                                                       ð
                                                                                                                                                                                                               qq
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the burspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTHE THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.
PTH: IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND
TO A FRAGMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE
METALLOPROTEINASE, DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matrix (By similarity).
-i. TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is widely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 origin.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE I DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
45-JUN-2002 (Rel. 41, Last annotation update)
45-JUN-2002 (Rel. 41, Last annotation update)
46-JUN-2012 precursor (10 34 24 - 1) (A disintegrin and metalloproteinase with thrombospondin motifs 12) (ADAM-TS 12) (ADAM-
SUBCELLULAR LOCATION: CYTOPLASMIC. PROBABLY BINDS INDIRECTLY TO THE INNER PLASMA MEMBRANE. SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                  EMBL; AB006784; BAA22056.1; -.

R EMBL; AL358552; CAB90788.1; -.

AR EMBL; AL132839; CAB60521.1; -.

AR Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil.

FT DOMAIN 1217 1252 COILED COIL (POTENTIAL).

Pur DOMAIN 1984 2012 MICROTUBUE-BINDING (POTENTIAL).

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed in gastric carcinomas and in cancer cells of diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1; Length 4196;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
8F10AE370184FC0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484308 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1140 SEHLLNELDDTHSSLSTVD 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 TEHXVXXLPDXHXXLXXXD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 36.8
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2169
2174
2520
4196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AT12_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADAMTS12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
NP_BIND
NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P58397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AT12_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
```

ö

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

8 November Run on:

2002, 19:24:14; Search time 10.4967 Seconds (without alignments) 1153.796 Million cell updates/sec

US-09-840-743-73

Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q09332 dro	3290 schiz	8397	salmc	91	Ol0339 orgyia pseu	Q9y910 aeropyrum p	treponema	aquifex ae	Q46839 escherichia	Q01631 neurospora	Q19869 caenorhabdi	Q9uzv4 pyrococcus				Q00461 fremyella d			Q9gqn0 drosophila	Q50864 myxococcus			-	_	-	P44689 haemophilus	Q10990 schizosacch	-	829	22492	3651	Q59934 streptococc
SUMMARIES	OI .	UGGG_DROME	DYHC_SCHPO	AT12_HUMAN	MUTS_SALTY	PIK1_YEAST	VCG3_NPVOP	TDXH_AERPE	MURF_TREPA	GUAA_AQUAE	GLCA_ECOL1	CYAA_NEUCR	RL26_CAEEL	TDXH_PYRAB		- 1	DVR1_BRARE	T701_FREDI	DRTS_TRYCR	TSCC_PSEAM	RP16_DROME	RFBC_MYXXA	ANK2_HUMAN	TYRC_ZYMMO	SEST_CAEEL	- 1	RFAY_SALTY	MESJ_HAEIN	YE0J_SCHPO		CNE1_HUMAN	HEXA_CAEEL	I10R_HUMAN	PFL_STRMU
	DB	Т	-	П	-	П	Н	Н	Н	-	П	<b>~</b>	Н	Н	H	Н	Н	mi	Н	Н	Н	7	٦	-	-	-	-	Н	7	7	-	-	П.	-
	Length	1548	4196	1593	855	1066	249	250	459	510	260	2300	142	216	216	. 332	355	380	521	1023	1098	1275	3924	293	517	190	232	430	490	492	537	552	578	77.5
df	Query Match	•				•	•	•		•																		5.4	5.4				5.4	5.4
	Score	41	38	37	36	36	34	34		34		34	33	33	33	33	33	33	33	33	33	33	n	32.5	'n	32	32	32	32	32	32	32	35	3.5
	Result No.	1	7	°.	4	2	9	7	æ ,	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	5. 5.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

032797 ]actocociis	032799 lactococcus	P41511 ustilago ma	Q61789 mus musculu	O30409 b tyrocidin	P42672 avian adeno	Q45557 bacillus sp	P55618 rhizobium s	026518 methanobact	Q44470 agrobacteri	P70786 agrobacteri	Q01767 streptomyce	
DET. LACT.A	PFL_LACLC	TOP1_USTMA	LMA3_MOUSE	TYCC_BACBR	ADEN_ADEG1	TRUA_BACSP	Y4PM_RHISN	APG2_METTH	TUB4_AGRVI	TUB3_AGRVI	LAT_STRCL	
-	-	-	٦	7	٦	Н	-	Н	Н	Н	П	
787	787	1019	2569	6486	206	244	272	402	433	449	457	
4	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.3	
33	32	32	32	32	31	31	31	31	31	31	31	
3.4	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

UGGG ID AC DT DT DT	UGGG_DROME STANDARD; PRT; 1548 AA.  ID UGGG_DROME STANDARD; PRT; 1548 AA.  Q09332; OCCUPATION STANDARD; PRT; 1548 AA.  Q10332; OCCUPATION STANDARD; PRT; 1548 AA.  Q10332; OCCUPATION STANDARD; PRT; 1548 AA.  Q10332; OCCUPATION STANDARD; PRT; 1548 AA.  Q103332; OCCUPATION STANDARD; PRT; 1548 AA.	STANDARD; (Rel. 35, Cr (Rel. 35, La (Rel. 41, La	RD; Created) Last seq Last ann ein gluco	PRT; 1548 AA. ed) sequence update) annotation update) ucosyltransferase	1548 Pupdate		precursor (EC 2.4.1)
GN	(UDP-G1c:glycoprotein glucosyltransferase) (dUGT). UGT OR UGGG.	coprotein	gluco	syltransi	erase)		
S O O	Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Mand	elanogast etazoa; A	er (Fri rthrop	lit fly). oda; Mano	libulat	a; Pancrus	tacea; Hexapoda;
88	Insecta; Pte	rygota; N Ephydroi	eoptera	a; Endopt rosophili	erygot	a; Diptera	; Brachycera;
0 X 2	NCBI_TaxID=7	227;			2		NCBL TaxID=7227;
R P	SEQUENCE FROM N.A., AND SEQUENCE OF	M N.A., A	ND SEQ	JENCE OF	23-37.		
S S	TISSUE=Embryo;	0; 6777. pub	Mod-77	, 00 7 00			
RA RA	MEDLINE 93240/22; FUDMEC 1/29408; Parker C.G., Fessler L.I., Nelson	o/22; Fun Fessler	Med=// L.I., _	Nelson R	E., Fe	ssler J.H.	•
RT	"Drosophila	UDP-gluco	se:gly	coproteir	glucc	syltransfe	rase: sequence
RT	and characterization of an enzyme that distinguishes between denatured and native proteins.":	rization d native	of an o	enzyme tl	at dis	tinguishes	) between
RL	EMBO J. 14:1	294-1303(	1995).				
ပ္ပ	-i- FUNCTION	FUNCTION: UNFOLDED, DENATURED GLYCOPROTEINS	D, DEN	ATURED GI	YCOPRC	TEINS ARE	ARE SUBSTANTIALLY
ຍູ	BETTER S	BETTER SUBSTRATES FOR GLUCOSYLATION BY THIS	FOR G	LUCOSYLAT	TION BY		ENZYME THAN ARE THE AND TRANSTENT
ဗ္ဗ	GLUCOSYL	ATION MAY	BE IN	VOLVED IN	I MONIT	ORING AND	GLUCOSYLATION MAY BE INVOLVED IN MONITORING AND/OR ASSISTING THE
ပ္ပင္ပ	FOLDING	FOLDING AND ASSEMBLY	BLY OF	NEWLY MA	NDE GLY	COPROTEINS	FOLDING AND ASSEMBLY OF NEWLY MADE GLYCOPROTEINS, IN ORDER TO
38	CHAPERONES.	ES.	CHITT	THE NEED	21000	TOWER IN E	OLDING FROM
ပ္ပ	-	: REQUIRE	S CALC	IUM AND N	IANGANE	SE IONS FC	REQUIRES CALCIUM AND MANGANESE IONS FOR ACTIVITY.
ပ္ပ ဗ	,	PATHWAY: Glycosylation.	ation.				
3 5		SUBUNIT: MONOMER. SUBCELLUTAR LOCATION: Endomlasmic reticulum	TON	idoplasmi	reti	milia	
ဗ္ဗ	1	ENTAL STA	GE: IS	PRESENT	AT LOW	BUT DETEC	DEVELOPMENTAL STAGE: IS PRESENT AT LOW BUT DETECTABLE LEVELS IN
ပ္ပ	THE EARL	IEST EMBR	YOS, II	NCREASING	3 AT 6	8 HRS WITH	THE EARLIEST EMBRYOS, INCREASING AT 6-8 HRS WITH A MAXIMUM AT 10
ပ္ပင္ပ	12 HRS.	LEVELS DE	CREASE	THEREAF	ER AND	12 HRS. LEVELS DECREASE THEREAFTER AND ARE NOT DETECTED	DETECTED IN 18-20
3 5	CECOND I	HKS EMBKIUS AND FIRST INSTA	DIIDATI	NSTAK LAR	WAE BU	T IS DEIEC	RES EMBRICS AND FIRST INSTAR LARVAE BUT IS DETECTED AGAIN AT
3 8	-!- SIMILARI	TY: SOME,	TO YE	AST KRE5,	S.TYE	SIMILARITY: SOME, TO YEAST KRE5, S.TYPHIMURIUM RFAJ AND	FAJ AND E.COLI
ပ္ပ	RFAI PRO	RFAI PROTEINS.					
ی ز	This curecin	SMISS-BBOM ONE :		· +		Troops of t	T+ to produced through a collabora
ָ ט ט	hetween the	Swiss In	stitute	of Bioi	nforma	tics and	the EMBI, outsti
ဗ္ဗ	the European	Bioinfor	matics	Institut	e.	ere are no	the European Bioinformatics Institute. There are no restrictions on
ខ្ល	use by non	non-profit	instita	institutions as long	long	as its content	ntent is in no
ည	modified and	this sta	tement	is not r	emoved	. Usage	Ö
ပ္ပ	entities req	uires a I	icense	agreemer	t (See	http://ww	w.isb-sib.ch/an
ე <u>წ</u>	or send an e	mail to I	1cense	1.SD-S1D.	ch).	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
200	FMBI: U20554: AAA85850.1:	. AAAB585	0.1:				
D.R.	FlyBase; FBqn0014075; Uqt.	00014075;	Uqt.				
DR	InterPro; IP	IPR002495;	GT_8.				
DR	Pfam; PF0150	1; Glyco_	transf_	-8; 1.		,	Pfam; PF01501; Glyco_transf_8; 1.
ΚW	Signal; Trans	sferase;	Glycos	/ltransfe	rase;	Endoplasmi	c reticulum;

THIS PAGE BLANK (USPTO)

17.6

```
395 ACAGITCIGCITITGGAAAGGATTCGTATGTGTCCGTGGATTCGAACAGAAGACAAAGAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cugi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon.
                                                                                                                                                                                                                                             6844 tctaacaaa 6852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                       TCTAACAAA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                    tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225
                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                              æ
                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                 6605
                                                                                                                                       6725
                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                           RESULT
BG123849
LOCUS
                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                δ
                                                        g
                                                                                   ŏ
                                                                                                           g
                                                                                                                                      ò
                                                                                                                                                              g
                                                                                                                                                                                         δ
                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                            EST 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 575)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                               AV545791 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cons Columbia Arabidopsis thaliana AV545791 AV545791.1 GI:8717205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                       6484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acagttctgcttttggaaaggattcgtatgtgtccgtggattcgaacagaagacaagagc 6604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
6365 gagaggaagttttccgctcaacgggacatatttccaagtcaacgagttatttgcagacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6425 cgagtccagtctcaaacccatcgatgttcctagagattggatatgggatctcccaagaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Arabidopsis thaliana roots Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

    .575
    /organism="Arabidopsis thallana"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 477; DB 9;
Pred. No. 4.7e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref-"taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone-"RZL01d12F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Columbia'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488; Conservative
                                                                                                                                                                                                                                                                                                                      thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                             1600 aaagga 1605
                                                                                                                                                                      481 NAAGGA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                         AV545791/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                      1480
                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6545
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
              셤
                                      à
                                                                                          ò
                                                                                                                  a
                                                                                                                                              ò
                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
759 bp mRNA linear EST 31-JAN-2001
EST469495 tomato shoot/meristem Lycopersicon esculentum cDNA clone
CTOF3624 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
                                                                                            6724
                                                                                                                                                                                                                                                             1. (bases 1 to 759)
van der Hoeven, R. Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Ronning, C. and Tanksley, S.
Generation of ESTs from tomato shoot/meristem tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6665 ctaaagatgactggaagaaagcaaacgcattgcttctctgctctcctctatttaaagcca
                                                                                                                          275 CTAAAGATGACTGGAAGAAAGCAAACGCATTGCTTCTCTGCTCTCCTCTATTTAAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1.759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="tomato shoot/meristem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 410; DB 10;
Pred. No. 3.5e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="cTOF3G24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG123849.1 GI:12624037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.0
Best Local Similarity 73.4
Matches 524; Conservative
```

ö

```
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30URCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                      밁
                                                                                                  Ъ
                                                                                                                     Š
                                                                                                                                              밁
                                                                                                                                                                ð
                                                                                                                                                                                          밁
                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              Matches 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                               516 tttcggagagttaggtgagtgttatttggggtgaggtagtgataaggtttgaagggggag
                                                                                                                                                                                                                                                                                   440 CAAGTCAGATTAAAAAGGAGTGTTCGTCCCTGTTGCTTTTGTTTTTGGTGTTTTGGAGAGAGT 381
                                                                                                                                                                                                                                                                                              456 caagtcagattaaaaaggagtgttcgtccatgttgctttgttttggtgttttggagagagt
                                                                                                                                                                                                                                         380
                                                                                                                                                                                           320
                                 816
                                                                                                                          969
                                                                                                   200
                                                                                                                                                 260
                                                                                                                                              TTTCGGAGAGTTAGGTGAGTGTTATTTGGGGTGAGGTAGTGATAACGTTTGAAGGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                     1 (bases 1 to 500)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and
                       tttgatcatggtgctcatcagggcgttaccaacttaagtatgatgatcaatagcttagcg 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis Genomic Sequencing. Update Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A BAC End Sequence Database for Identifying Minimal Overlaps in
          Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Steve Rounsley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rounsley@tigr.org
Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute for Genomic Research
2 Medical Center Dr., Rockville,
301 838 0200
301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 500.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII
; produced by Rod Wing"
; 138 c 70 g 133 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T1907"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="TAMU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 500
                                                                                                                                                                                                                                                                                                                                                                                           7.28;
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Score 493.6; DB 1
Pred. No. 9.6e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20850, USA
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Venter
                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Golden, K.
                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                      575
                     21
                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
B28303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                            밁
                                                                                                                                                                              δÃ
                                                                                                                                                                                                       В
                                                                                                               g
                                                                                                                                   Š
                                           δõ
                                                                   망
                                                                                         Š
Ş
                       В
```

gacatgcacaagcttg

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                            Best Local
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                           20
                                                                                                                                                                                       1300
                                                                                                                                                                1240
                                                                                                                                   121 ATTAGAATATCTTAAGAAAGTCATGGTTTTGAACAGATGGACCTCCAGCGTGTAACAAGC
                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     attagaatatottaagaaagtcatggttttgaacagatggacctccagcgtgtaacaagc 1299
ttgaacagatagttacaactactggacatgaaatcccagagccgaaatctgacaaaagta 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B28303 480 UP
T9J15TRB TAMU Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                  481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis Genomic Sequencing Unpublished (1997) Other_GSSs: T9JT5TFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              в28303.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a BAC End Sequence Database To Identify Minimal Overlaps for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rounsley, S.D., Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Steve Rounsley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rounsley@tigr.org
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ass: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute for Genomic Research
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis t
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T9J15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:2514269
                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII; Produced by Rod Wing" 138 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .486
                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="TAMU"
                                                                                                                                                                                                                                                                                                                 7.0%;
                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                   Score 478.6; DB 1
Pred. No. 2.7e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        486 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rockville,
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA linear GSS 13-OCT-1997 genomic clone T9J15, DNA
                                                                                                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20850,
                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                  Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                180
                                                                 1419
```

of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asam/zu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/. Location/Qualifiers

/organism="Arabidopsis thaliana"

/db_xref-"taxon:3702"

/clone="SQ049d09F" /strain="Columbia

The First Laboratory for Plant Gene Research Kazusa DNA Research Institute

20363093 Contact: Erika Asamizu

/clone_lib="Arabidopsis thaliana green siliques Columbia" /tissue_type="green siliques" /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:

142 t

112 9

113 c

ď 160

```
2002
08:44:45
```

```
source
                              JOURNAL
MEDLINE
                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                       9689
                                                                                                                                                                                                                                                                                                                              9159
                                                                                                                                                                                                                                                                                                                                                          9259
                                                                                                                                                                                                                                                                                                  6456
                                                                               FEATURES
                                            COMMENT
                                                                                                                                                            ORIGIN
                                                                                                                                                                                                             à
                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                ij
                                                    SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                 6312 gcaaactcacagacagttcgaggaactcttctgataccttgtcggactgccatgagaga 6371
                                                                                                                                                                                                                  6551
                                                                                                                                                                               agicicaaacccaicgaigitcciagagaitggaiatgggaictcccaagaaggacigit 6491
                                                                                                                                                                                                                                               6611
                                                                                                                                                                                                                                                                          6671
                                                                                                                              6731
                                                                                                                                                                                                                                                                                                                                                      384
                                                                                                                                                                                                                                                            324
                                                                                                                                                                                                                                                                                              tacttcggaacatcagtaacatcaatattcagaggtctttcaacggagcagatacagttc
                                                                                                                                                                                                                                       tgcttttggaaaggattcgtatgtgtccgtggattcgaacagaagacaagagcaccgcgt
                                                                                                                                                                                                                                              6612 ccattaatggcaaggttgcatttcctgcgagcaaattgaagaacaacaaaacctaaaga
1. .623
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="RzL05c12F"
/clone="RzL05c12F"
/flosu=Lib="Arabidopsis thaliana roots Columbia"
/fissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: ECORI;
                                                                                                                ij
                                                                                                Length 623;
                                                                                                              Indels
                                                                                             Score 528.4; DB 9;
Pred. No. 1.9e-76;
0; Mismatches 1;
                                                                  184
                                                                  6
                                                                  135 (
                                                                                           7.7%;
                                                                127 c
                                                                                                        540; Conservative
                                                                                                   Similarity
                                                                177
                                                                                                                                                                                                                                                                                                                                                                                    6851 aa 6852
                                                                                          Query Match
Best Local S
Matches 540
                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                  83 AA
                                                              BASE COUNT
ORIGIN
                                                                                                                                                                               6432
                                                                                                                                                                                                           6492
                                                                                                                                                                                                                                       6552
                                                                                                                                                                                                                                                                                                                           6732
                                                                                                                        ò
                                                                                                                                                  à
                                                                                                                                                                임
                                                                                                                                                                               ò
                                                                                                                                                                                           d
                                                                                                                                                                                                           à
                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                      GSS 21-NOV-1997
                                                                       6395
                                                                                                         6455
                                                                                                                                  agagattggatatgggatctcccaagaaggactgtttacttcggaacatcagtaacatca 6515
                                                                                                         Gaps
                                                                                                                                          9
                                                                                                                                                                                                           ttccaagtcaacgagttatttgcagaccacgagtccagtctcaaacccatcgatgttcct
                                                                                                                                                                 giccgiggaitcgaacagaagacaagagcaccgcgitccaitaaiggcaaggitgcaiitt
                                                                                                                                                                                                                                   6636 cctgcgagcaaattgaagaacaacaaacctaaagatgactggaagaaagcaaacgcatt
                                                                                                                                                                                                                                                                    6696 gottototgototoototatttaaagocaggaaaagtoccatttagacataataacagga
                                                                                                                                                                                                                                                                              B60854 11907TF TAMU Arabidopsis thaliana genomic clone T1907, DNA
                     ;
0
   DB 9; Length 527;
                    Indels
                                                                                                                                                                                                                                                                                                    Score 525.4; DB 9
Pred. No. 6.2e-76;
                 0; Mismatches
7.68;
99.88;
                                                                                                                                                                                                                                                                                                                                                                                 sequence.
B60854
B60854.1 GI:2627785
              Matches 526; Conservative
       Similarity
Query Match
       Best Local
                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                               RESULT
B60854/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                     óλ
                                                                                                                                                                                                                                                                                                                    g
```

EST 06-SEP-2000

AV556668 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana green siliques Columbia Arabidopsis

DEFINITION ACCESSION VERSION

AV556668

AV556668.1 GI:8728083

Arabidopsis thaliana

thale cress.

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 527)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

v 0 v 0 0 v 0 0 v

IntelliGenetics

Results file seq72-t48453.res FastDB - Fast Pairwise Comparison Release 5.4

made

by bobryen on Tue 17

Dec 102 12:58:03-PST

(1-151)

of Sequences

```
Similarity matrix PA
Threshold level of sim.
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                                                                                                                                                                          SCORE
                                                                                                                                                                                                                                                                    SECZECOES
                                                                                                                                                                                                                                                                                                                                                         ۳ O
                                                                                                                                                                                                                                                                                                                                                                                   2 E B Z C Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query sequence being compared: SEQ72-T48453 Number of sequences searched: Number of scores above cutoff:
                                  Number
Number
Number
The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                              Times:
                                                                                                                                          Randomization group
                                                                                                        Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100-
                                                                                                                                                                                                                                                                                                                                                           10-
                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Results of the initial comparison of SEQ72-T48453 (1-151) with: File : seq72compares.pep
                                  266
                                  residues:
sequences searched:
scores above cutoff:
                                                                                                                                                                                                                                                   128
                                                                      00:00:00.00
                                                                                                                                                                                      PAM-150
                                                                                                Mean
87
                                                                                                                                                             5.00
0.05
                                                                                                                                                                                                                                                   42
                                                                                                                                           0 1
                                                                                                                          SEARCH STATISTICS
                                                                                                                                                                                                                PARAMETERS
                                                                                                                                                                                                                                                   56
                                                                                                                                                                                              K-tuple
                                                                                                                                                                    Joining penalty Window size
                                                                                                 Median
42
                                                                                                                                                                                                                                           0 6 -
                                                                                                                                                                                                                                                   83-
                                                                      Total Elapsed 00:00:00:00.00
                                                                                                Standard Deviation 43.25
                                                                                                                                                                                                                                                    97
                                                                                                                                                                    20
151
                                                                                                                                                                                                                                                    125
```

×

identical

sequence

ç

the

query sequence was

not found

The list of best scores is:

Initial Score Residue Identity Gaps  KSKESAKSTOKK 780 780 60 FLXXXVXXHGXID 11 11 FLNRLVKHGSID 850 860	1. SEQ72-T48453 q9sr66	1. q9sr66 22t48453 4	Sequence Name
125 Optimized Score  523 Matches 0 Conservative Subst 0 Conservative Subst 10 20 WDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	(1-151) T22Kl8.18 protein.	T22K18.18 protein. TOIG of: t48453 check: 2431	Description
137 Signifi 80 Mismatc 15tutions 30 20XXXXXXXXXXXXXXXI 30 B30 30 B20 B30 110 B20 110 B		1309	Init. Opt. Length Score Score
Significance Mismatches Mismatches XXXXXXIXXGM		125 124	Init. Opt.
cance - hes - 1/40 AT ATTEMPT		137 134	Opt. Score
0.88 68 50 7 7 7 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8		0.88	Sig.
K X X		00	Sig. Frame

Initial Score Residue Identity 25.3g072-748453 (1-151) "汽车8453分 TOIG of: t48453 check: 2431 from: 1 PLPDELOMHLLELYELHYHMITFGKVFCTKVKPNCNACPMKAECRHY 920 930 940 X 950 960 130 PLPXYLOLHILEXYPXXXXXQKXLWPR |||*,||||||| ||| PLPESIOLHILEI || 550 x 8 E A 124 61**%** 0 Optimized Score = 134
Matches = 84
Conservative Substitutions 134 84 Significance Mismatches ë: 0.86 53 0

PLPXXLQLHLLEXYPXXXXXQKXLMPR

DNA-(apurinic or a probable endonucle A/G-specific adeniadenine glycosylas adenine glycosylas DNA-(apurinic or a cystatin D precurs endonuclease III Pendonuclease III endonuclease III Pendonuclease III Cendonuclease III Cendonuc

D98016 G96984 B38535 E9108 H85953 A647142 A47142 E82780 H83208 F72387 D70316

us-09-840-743-72.rpr

```
2209
2211
2211
2212
2212
2213
3260
3260
355
2002, 19:24:14 ; Search time 15.0327 Seconds (without alignments) 1470.857 Million cell updates/sec
                                             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                   OM protein - protein search, using sw model
                                         US-09-840-743-72
                          œ
                          November
                                             Perfect score:
                                                 Sequence:
                          on:
```

## ALIGNMENTS

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* PIR_73:*

Database

283224 seqs, 96134422 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

ж. ç,

T48453	
hypothetical protein T32M21.170 - Arabidopsis thaliana	iana
C;Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 20-Apr-2000	#text change 20-Apr-2000
C; Accession: T48453	
R; Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck,	C.; Dasseville, R.; De Clerck,
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.	
submitted to the Protein Sequence Database, March ;	2000
A; Reference number: Z24487	
A; Accession: T48453	
A;Status: preliminary	
A; Molecule type: DNA	
A; Residues: 1-555 <bev></bev>	
A;Cross-references: EMBL:AL162875	
A; Experimental source: cultivar Columbia; BAC clone T32M21	e T32M21
C; Genetics:	
A; Map position: 5	
A; Introns: 469/3; 496/2; 524/3	~~**
A; Note: T32M21.170	
Ouery Match	: Lenath 555;
Similarity 44.58;	
ative 0; Mismatches	61; Indels 10; Gaps 1;
Qy 18 DXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	XXXXXFLXXXVXXXGXIDLE 77
DD 436 DSIDYEAIRRASISEISEAIKERGMNNMLAVRIKDFLERIVKDHGGIDLE	KDFLERIVKDHGGIDLE 485
Oy 78 WLRXXXXXXXXXXXXXCXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLP	DINVGRIXVRXGXVPLXPLP 137
Db 486 WLRESPPDKAKDYLLSIRGLGLKSVECVRLLTLHNIAFPVDTNVGRIAVRMGWVPLOPLP 545	DINVGRIAVRMGWVPLOPLP 545

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	prot prot iii iiii iiii iiii nucl	DNA-(apurinic or a probable endonucle probable endonucle endonuclease III endonuclease III endonuclease III (probable DNA-(apur endonuclease III (endonuclease III (endonuclea
SUMMARIES ID	T48453 T05430 D84781 D75275 S7573 S7573 G87199 B69202 F71025 C75459 F72383	AGB6/38 AF11683 B71919 A64593 H76959 H76255 B83862 C69461 I40525 C69461 C697149 B75537 C87149
DB	00000000000000000	
Length	555 2017 2017 2017 2017 2017 2017 2017 2017	218 219 219 218 218 218 218 219 210 210 212 222 232 292
å Query Match	2222 2222 22222 22222 22222 22222 22222 2222	
Score	20 20 20 20 20 20 20 20 20 20 20 20 20 2	69 69 69 69 69 69 69 69 69 69 69 69 69 6
Result Nõ.	1 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	115 116 117 128 128 128 128 138

138 XXXQXHXL 145 | | | 546 ESLQLHLL 553

원 δ

RESULT 2
106430

Hypothetical protein F28A23.180 - Arabidopsis thaliana
C;Species: Arabidogsis thaliana (mouse-ear cress)
C;Dectes: Arabidogsis thaliana (mouse-ear cress)
C;Accession: 176430
R;Bevan, M; Weichselgarther, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.
S;Revan, M; Weichselgarther, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.
S;Recession: T15415
A;Recession: T05430
A;Molecule type: DNA
A;Recidues: 1-917 <BEV>
A;Recidues: 1-917 <BEV>
A;Recidues: 1-917 <BEV>
A;Experimental source: cultivar Columbia; BAC clone F28A23

C; Superfamily:

```
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cha A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardhoois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Massuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
T48452
Hypothetical protein T32M21.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48452
N : Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: E69958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein yahB - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, March 2000 A;Reference number: Z24487 A;Accession: T48452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 5
A; Introns: 167/1; |
A; Note: T32M21.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: cultivar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; McLecule type: DNA
A; Residues: 1-1017 <BEV>
A; Cross references: EMBL; AL162875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                      Status: preliminary; nucleic acid sequence not shown; translation; Molecule type: DNA; Mesidues: 1-442 < KUN>
Cross-references: GB:299116; GB:AL009126; NID:g2634723; perimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KVXXDXXTXXXWXXLXXXXXXXXXX------XXERXXFXXRXXXFIXRMXXXQG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KVXXDXXTXXXXXXL-----XXXXDXXXXXXXXXXXXFXXXFXXRXXXFIXRMXXXQGXRX 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVDIDDETTRIWNLLMGKGDEKEGDEEKDKKKEKWWEEERRVFRGRADSFIARMHLVQG 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKQWKGSVVDSVVGVFLTQNTTDYLSSNAFMSVAAKFP 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLQGNRK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity 28.8
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana hypothetical protein F28A23.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              874/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.0%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Columbia; BAC clone T32M21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49.5; D
Pred. No. 5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 162; DB 2;
Pred. No. 3.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                     PIDN:CAB14406.1; PID:g2634909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                               not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Clerck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De
```

RESULT T06602

В

744

FDKYAGSTYDSALGLFLT 761

```
Ω<sub>γ</sub>
                                                                                                                 A; Gene: UU557
A; Genetic code:
                                                                                                                                                                      A;Cross-references: GB:AE002154; GB:AF222894; NID:g6899557; A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1131 <GLA>
                                                                                                                                                                                                                                                                   A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views A;Reference number: A82870 A;Accession: F82875
                                                                                                                                                                                                                                                                                                                         R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein UU557 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_chang.
                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: yqhB
C;Superfamily: hypothetical protein HI0107
                                                                                                                                                                                                                                                                                                                                                 R;Glass,
                                                                                                                                                                                                                                                                                                                                                               C; Accession: F82875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 45/1; 105/2; 199/3; 303/2; 382/3; 503/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, March 1995
A;Reference number: 220465
A;Accession: T28069
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ZK892.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z48638; PIDN:CAA88567.1; GSPDB:GN00020; CESP:ZK892.3 A;Experimental source: clone ZK892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-541 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
                                                         Query Match
Best Local
                                         Matches
                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 RTFSNWANARILVVFVAFITRRWDTASYVCAAISALIFP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 VDTLGGWFLTQNIDAEPESA 415
                                       Local Similarity
nes 9; Conserv
54 FXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 RXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 VDSVXGVFLTQNXDXXSSXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CESP: ZK892.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.18;
                                                     16.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.18; 28.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                     Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 2; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; L
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.5;
                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                            #text_change
                                                                       Length 1131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                    PIDN:AAF30970.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                            20-Aug-2000
                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

## GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

8, 2002, 19:24:14; Search time 5.88235 Seconds (without alignments) 1470.857 Million cell updates/sec November

US-09-840-743-71 Title: Perfect score:

275
1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 : Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	hypothetical prote hypothetical prote hypothetical prote conserved hypothetical prote probable periplasm aminopeptidase N V probable phosphopr probable phosphopr hypothetical prote early protein gpl3	hemolysin homolog hypothetical prote
SUMMARIES	04040404040404040404040404040404040404	F69826 T24676
DB		0.01
Length	1207 1917 1917 1917 1133 133 133 133 133 133 133 133 133	444 638
% Query Match		14.9 14.9
Score	0164 44 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 0107 01	41
Result No.	110 m 4 m 0 L 8 0 0 110 110 110 110 110 110 110 110 1	2 5 E

myosin IC - slime RNA polymerase bet probable lectin pr	gellan lyase (EC 4 preprotein translo conserved hypothet	hypothetical prote spoU rRNA methylas probable sugar ABC	citrate (si)-synth citrate synthase, qlucan 1,4-alpha-q	hypothetical prote probable heterochr	wp-40 repeat prote hypothetical prote
T30578 S73652 T40912	T00047 E95237 F98101	B72776 G87396 AG0404	S41563 T49379 T49633	T23238 T37916	T00637
222	000	0 3 8	000	909	20
1181	2475 99 99	12 26 32	469 469 748	96	1922
14.9	14.7 14.5 14.5	14.5	14.5 14.5 14.5	14.5	14.5
41 41 40.5	40.5	4 4 4 0 0 0	444	444	4 4
30 31 32	3 3 3 5 4 5 5 5	36 37 38	39 40 41	44.3	45

## ALIGNMENTS

RESULT 1  Begin to the many statements of the month of th
--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

IntelliGenetics

Results file seq72-q941x6.res

made by

bobryen on

Tue

17 Dec 102 12:58:40-PST

Release FastDB -

G

Fast Pairwise Comparison of Sequences 5.4

٦,

```
Number
Number
Number
                                                                                                                                   Similarity matrix
Threshold level of sim.
Mismatch penalty
                                                                                                                                                                                                                           SHCZHCOHS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query sequence being compared: SEQ72-Q941X6 Number of sequences searched: Number of scores above cutoff:
                                                                                                                                                                                                 SCORE
STDEV
                                          Times:
                                                                                                   Cutoff score
Randomization group
                                                                                                                    Gap size penalty
                                                                                                                             Gap penalty
                                                                   Scores:
                                                                                                                                                                                                                                                                                                                                                                                                  100-
                                                                                                                                                                                                                                                                                                                                                                         50-
                                                                                                                                                                                                                                                                                                               5
r of residues:
r of sequences
r of scores abo
                                                                                                                                                                                                                                                                                                                                                                                                                  Results of the initial comparison File: seq72compares.pep
sequences searched: scores above cutoff:
                                                                                                                                                                                                          =-
                                                                                                                                                                                                           22-
                                 CPU
00:00:00.90
                                                                                                                                              PAM-150
. 16%
                                                           Mean
69
                                                                                                                     5.00
0.05
                                                                                                                                                                                                           ω--
                                                                                                     0 1
                                                                                    SEARCH STATISTICS
                                                                                                                                                                        PARAMETERS
                                                                                                                                                                                                          4-
                                                                                                                             Joining penalty Window size
                                                                                                                                                      K-tuple
                                                           Median
30
3817
5
5
                                                                                                                                                                                                  0 | 56
                                                                                                                                                                                                                                                                                                                                                                                                                           of SEQ72-Q941X6
                                 Total Elapsed 00:00:01.00
                                                           Standard Deviation 36.96
                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                          (1-132) with:
                                                                                                                                                                                                   89
                                                                                                                             20
132
                                                                                                                                                                                                          100
                                                                                                                                                                                                                                     *
```

The list of best scores is

100% identical sequence to

the

query sequence was

The scores below are sorted by initial score. Significance is calculated based on initial score.

Initial Score Residue Identity - Gaps Gaps 1. q9sr66 2. t48453 行為可**941**x6行為 Residue Identity = Gaps = Initial Score - Residue Identity -۲ 3.<u>にSEO72</u>70941X6 (1-132) ^常有941X6 Putative FPPsynthasel (Fragment). Initial Score Sequence Name MKGTLADGKKPTSQWDS\LRKDVEGNEGRQERNKNNMDSIDYEAIRRAS SEQ72-Q941X6 (1-132) q9sr66 T22K18.18 protein SEQ72-Q941X6 (1-132) t48453 TOIG of 130 X LPDELQMHLLELYELHYHMITFGKVFCTK
930
940 SKESAKSTOKKSVDWDS#RKEAESGGRKRERTERTWDTVDWDALRCTDVHKIANL/LIKRGMNNMLAERIKAF
780 790 800 810, 820 830, 840 LPESLOLHLLEL 550 X LPXXXQXH A ... 130 60 Description T22K18.18 protein.
TOIG of: t48453 check: 2431
Putative FPPsynthasel (Fragme £4.8453 Optimized Score = 115
Matches = 72
Conservative Substitutions Optimized Score 121 Significance Matches 75 Mismatches Conservative Substitutions Optimized Scor Conservative 90 10 check: 24 90 Substitutions 20 from: 1 119 73 100 Init. Opt. Length Score Score ASISEISEAIKERGMNNMI 450, AFO 1309 555 119 Significance Mismatches Mi ignificance 8 100 96 93 110 40 121 119 115 . . . 0.73 58 1 Sig. Frame 0.84 0 0.73 0 0.65 0 **LAVRIKDE** 0 57 0 0 4 6 5 0 6 6 5 70 50 50

Asada T., Fukusaki E., Kobayashi A., Sando T.;
"Prenyltransferase of Euphorbia tirucalli.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR003265; Endo_3c.
Pfam; PF00730; HHH-GPD; 1.

RA RI DR DR DR DR FT

119 AA; 13771 MW; FBDBCE4CD0CC5B81 CRC64;

NON_TER SEQUENCE

ï

```
-;
                                930
                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudigotyledons; Core eudicots; Rosidae;
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 DSIDYEAIRRASISEISEAIKERGMNNMLAVRI------KDFLERIVKDHGGIDLE 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 WLRXXXXXX¥KXXLLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.,
Rudd S., Lemcke K., Mayer K.P.X.;
Submitted (MAR-2000) to the FemBL/GenBank/DDBJ databases.
                                    157 XLWPRICKLXQXTLYELHYXXIIFGKXXFCTKXXPNCNACPMXXXCXXXXSA 209
                                                     32.9%; Score 228; DB 10; Length 555; 44.5%; Pred. No. 1.6e-29;
EU Arabidopsis sequencing/project,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALI62875; CABB5563/1;
Interpro; IPR003265; Endo_3c.
Pfam; PF00730; HhH-GPD/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $2088 MW; AlB44BDDE17FDC1E CRC64;
                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
Hypothetical 62.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.6e
0; Mismatches
                                                                                                                                       PRT;
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 44.59
Matches 57; Conser/ative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00478; ENDO39, Hypothetical protein, SEQUENCE 555 AA; #2(
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 XXXQXHXL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546 ESLQLHLL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                 RESULT 2
                                                                                                                09LZ68
                                                                                                                                        ò
                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

04949.0)
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 106.3 kDa protein.
F28A23.180 OR AT4G3406.0.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II; Brassicaceae; Arabidopsis. 37 IXXRGXXXXLXXRIXXXXXXXXXXXXFLXXXVXXXGXIDLEWLRXXXXXXXXXXXLXXXG 96 31 IKBRGMNNVLAKRI------KDFLNRLVREHGNIDLEWLRDVPPDKAKEYLLSIRG 80 PXXXXXQKXLWPRLCKLXQXTLYELHYX 176 ō. -----YELHYQ 661 Herzl A. Gaps Bevan M., Weichselgartner M., Fartmann B., Granderath K., Dauner Herzl A., Neumann S., Hoheisel J., Jesse T., Heijnen L., Vos P., Schueller C.; Schueller C. DB 10; Length 917; [2]
SEQUENCE FROM N.A.
Weichselgartner M., Fartmann B., Granderath K., Dauner D.,
Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL021961; CAA17566.1; EMBL; AL161584; CAB80123.1; InterPro; IPR003265; Endo_3c. InterPro; IPR003565; FeS_bind Indels (02B3770ACE1A454 CRC64; Score 202; DB 10; Pred. No. 8.1e-26; 0; Mismatches 39; 97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXP 135 29.1%; Scord 201.5; DB 10; 49.5%; Pred No. 7.8e-25; tive 0; Mismatches 22; Score 202; 662 MITFGK-VFCTKTIPNCNACPM-KSECKYFASA 692 177 XITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 625 VDTNVGRIAVRLGLVPLEPLPNGVQMHQLFE-117 VDTNVGRIXVRXGXVPLXPLPXXXQXHXLXX 29.1%; 50.5%; Hypothetical protein. SEQUENCE 917 AA; 106310 MW; Conservative PRELIMINARY; SMART; SM00478; ENDO3c; 1. SMART; SM00525; FES; 1. Conservative Similarity SEQUENCE FROM N.A. Local Similarity ses 46; Conserv Local S... 50; Query Match 049498 Query Match Matches Matches ò g ŏ g δ Dp δ

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
Wall_TaxID=142860;

01-DEC-2001 (TrEWBLrel. 19, Created) 01-DEC-2001 (TrEWBLrel. 19, Last sequence update) 01-JUN-2002 (TrEWBLrel. 21, Last annotation update) Putative FPPSynthasel (Fragment)

Euphorbia tirucalli,

AC OS SE DIT

NUENCE FROM N.A.

119 AA.

PRELIMINARY;

094LX6 094LX6

> 0 < of lo intelligenetics > 0 <

Query sequence being compared: SEQ71-049498 (1-90)
Number of sequences searched:
4
Number of scores above cutoff:

Results file seq71-o49498.res made by bobryen on Tue 17 Dec 102 12:55:59-PST.

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

```
Similarity matrix PAThreshold level of sim. Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization group
                                                                                                                                                                                       SCORE
STDEV
Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                         Times:
                                                                Scores:
                                                                                                                                                                                                                                                                                                                                                                            .100
                                                                                                                                                                                                                                                                                                                                                     50-
                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                          Results of the initial comparison of SEQ71-049498 (1-90) with: File : seq71compares.pep
                                                                                                                                                                                           15-
                                CPU
00:00:00.00
                                                                                                                                       PAM-150
                                                         Mean
60
                                                                                                                                                                                         22 |
-5
                                                                                                                5.00
                                                                                                                                                                PARAMETERS
                                                                               SEARCH STATISTICS
                                                                                                                                                                                         29 |
-4
                                                                                                                                              K-tuple
                                                                                                                       Joining penalty
Window size
                                                         Median
56
                 4350
                                                                                                                                                                                        37
-3
                                                                                                                                                                                       -44
2
                                                         Standard Deviation 6.65
                                Total Elapsed 00:00:00.00
                                                                                                                                                                                       -12
                                                                                                                                                                                        0 59
                                                                                                                        20
90
                                                                                                                                                                                        16-
```

The list of best scores is:

A 100% identical sequence to the query sequence was not found.

The scores below are sorted by initial score. Significance is calculated based on initial score.

50 HXLQGN               RLQGN 470	LKINKK 400	Initial Sc Residue Id Gaps	2. <u>SEO71</u> ; 049498	HXLQGN          HRLQGN 470	LKINKK 400	Initial Score Residue Iden Gaps	1. SEQ71-049498 t05430	21	Sequence Name
RXFXQWKG	VTTMIKAD 410	Score - Identity -		RXEXQWKG	VТТМІКАЬ 4 1/0	Score = Identity =		983 84	! ! !
60 .GSVVDSVVGV                       GSVVDSVVGV 490	X KVX   *  KKLVTAKVN 420	70# 8	(1-90) Hypothetical 106.3	DWKGSVVDSVVGVFLTQN	X KKLVTAKVN 420	70# 8	(1-90) TOIG of: t(	TOIG of: t05430 Hypothetical 10	Description
50 70 80 90 HXLQGNRXFXQWKGSVVDSVVGVFLTQN-TDXLSSNAFMXVAAXFP	10 30 30 40 KVXILDETIXMYVLMXXDDKXTXAKWXXERXXEXTRXDLFINRN   12   1   12   1   1   1   1   1   1	Optimized Sc Matches Conservative		HXLOGURXEKQWKGSVVDSVVGVFLTQN-TDXLSSNAFMXVAAXFP		Optimized Sco Matches Conservative	t05430 che	t05430 c	on
80 90 	30 ADAITMANDS:	Scc 1ve	kDa protein.	80 KLSSNAFMXV           CLSSNAFMSV	ETXXXWXVLM ETIKEWDVLMVNDS 430		check: 9156	heck: kDa	
90 VAAXEP    :   VAAKEPVD	20 XXDDKI 1111 PSRSYDDKI	ore = 80 = 69 Substitutions	'n	VAAXEP	PŚRSYDDK	bre = 80 59 Substitutions	from:	9156 protei	Length
AREGLSYY 520	30 KTXAKWXXE ;   ;       ; ;   ETEAKWKKE 450	Significance Mismatches s		AREGLSYY 520	XTXAKWXX       ETEAKWKK	Significance Mismatches s	1 to: 9	917 66 917 66	Init. gth Score
IEEPQDAK 530	O ERXXEXTR   ::: :    ::: ::    :::	icance =		IEEPQDAK 530	30 XERXXEXTR         KEREIFQTR 460	icance =	917	6 80 80	Opt.
SS	20 30 40XXDDXXTXAKWXXERXXFXTRXDLFINRM	0.90 21 0		SS	20 40	0.90 21		0.90	Sig. Fr

Ä.

Herzl

Ω,,

RESULT 2

```
418 KVNLDPETIKEWDVLMYNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLQGNRK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXXERXXFXXRXXXFIXRMXXXQGXRX 53
                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO19161; CAA17566.1; -..
EMBL; ALI61584; CAB80123.1; -.
InterPro; IPR003545; Endo_3c.
InterPro; IPR003545; Eos. bind.
Pfam; PF00730; HhH-GPD; 1.
Mewes H.W., Mayer K., Schueller C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                             SEQUENCE FROM N.A.
Welchselgartner M., Fartmann B., Granderath K., Dauner I
Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                     11 protein.
917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 162; DB 10;
Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.0%;
nilarity 28.8%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                    58.9%;
43.9%;
                                                                                                                                                                                                                                                                                                           SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein
SEQUENCE 1017 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N. P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=370
                                                                                                                                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                     SÉQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09LZ69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9LZ69
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69ZT60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                              ARAIN-CV COLUMBIA;
MEDLINE=20083487; Pubmed=10617197;
MEDLINE=20083487; Pubmed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowmhn C.L., Barnstead M.E., Feldblyum T.V.,
Fujii C.Y., Katchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Buell C.R., Katchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Adams M.D., Carrera A.J., Carsay T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.; the plant Arabidopsis
thaliana ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLEEL. 06, Last sequence update)
01-JUN-2001 (TrEMBLEEL. 17, Last annotation update)
Hypothetical 106.3 Mon protein.
FSBA23.180 OR A74G34060.
Arabidopsis thaliana (Mouse-ear cress).
Rukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 KVDLDDETDRVWKLLLENINSEGVDGSDEOKAKWWEEERNVFRGRADSFIARMHLVQGDR 559
                                                                                                                                                                                                                                          Eukaryophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Bevan M., Weichselgartner M., Fartmann B., Granderath K., Dauner D.,
erzl A., Neumann S., Hoheisel J., Jesse T., Heijnen L., Vos P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---XXXXDXXXXXXXXXERXXFXXRXXXFIXRMXXXQGXR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. |
135916 MW; ADDB6C9EE94DDF67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006919; AAD24633.L; -.
InterPro; IPR003651; FeS. Bind.
SMART; SM00525; FES; 1.
SEQUENCE 135916 MW; ADDB6C9EE94DDF67 CRC64;
                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 163.5; DB 10;
Pred. No. 9.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1,7e-20;
nes 47;
                                   595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        917 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 59.5%;
1 Similarity 43.4%;
43; Conservative (
                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KVXXDXXTXXXWXXL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                              At2g36490 protein.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         049498
049498;
                                                                                                                                    902360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
049498
```

ä

Gaps

.,

Indels

47;

Length 917;

```
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              931 KVDIDDETTRIWNLLMGK&DEKEGDEEKDKKKEKWWEEERRVFRGRADSFIARMHLVQG
                                                                                                                                                                                                                                                                                                                                                                         Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Glelen J., Van Montagu M., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112139 MW; 4F7C313A891EC83F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162875; CAR85562.1;
01-0CT-2000 (prEMBLrel. 15, Created)
01-0CT-2000 (prEMBLrel. 15, Last sequence update)
01-0CT-2000 (prEMBLrel. 15, Last annotation update)
Hypothetical 12.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49.5;
```

δ

à

RESULT 5